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MPsrch_nn n.a. n.a. database search, using Smith-Waterman algorithm

Run on: Sun Oct 24 17:42:44 1999; MasPar time 465.47 Seconds 1393.481 Million cell updates/sec

Tabular output not generated.

>US-09-092-296-7 (51-284) from US09092296.seq

Description:
Perfect Score:
N.A. Sequence:
Comp: 51 ATGGGGTCTGGGCTGCCCCT......ACCATGTTGTCTGCAACACA 284
TACCCCAAGACCCGACGGGGA.....TGGTACAACAGACGTTGTGT

Scoring table: TABLE default Gap 6

Nmatch STD : Dbase 0; Query 0

646147 seqs, 1385953633 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

Database:

emb158
1:em_bal 2:em_ba2 3:em_fun 4:em_htg 5:em_huml 6:em_hum2
1:em_in 8:em_om 9:em_or 10:em_ov 11:em_pat 12:em_ph
13:em_pl 14:em_ro 15:em_sts 16:em_vi
genbankill
17:9b_bal 18:9b_ba2 19:9b_htgl 20:9b_htg2 21:9b_inl
22:9b_in2 23:9b_om 24:9b_ov 25:9b_pat 26:9b_ph 27:9b_pll
28:9b_pl2 29:9b_pr1 30:9b_pr2 31:9b_pr3 32:9b_ro
33:9b_st 34:9b_sts 35:9b_sy 36:9b_un 37:9b_vi

Statistics: Mean 9.653; Variance 4.972; scale 1.941

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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23	24	24	25	2 /	27	28	29	32	, ,,	4.8	92	Score	
9.8	10.3	10.3	10.7	11.5	11.5	12.0	12.4	13.7	14.1	20.5	39.3	Match	Query
1056	1056	0.00	5 0 5 U 5 U 5 U 5 U 5 U 5 U 5 U 5 U 5 U	216021	215	965	215	216021	74371	7218	47323	Match Length	
23	2 6	2,5	25	31	25	25	25	31	31	25	31	Bd	
MVU87256	MVII87256	A62080	E04076	HUAC004787	128278	AR024229	128278	HUAC004787	AC005369	I66494	AC005937	th gr	
Mustela vison GT dinuc	Mistala wices of Atom	Someon 1 for KIAA030	gDNA encoding envelope	Homo sapiens Chromosom	Sequence 5 from patent	Sequence 22 from paten	Sequence 5 from patent	Homo sapiens Chromosom	Homo sapiens chromosom	Sequence 14 from paten	Homo sapiens clone UWG	Description	
5.25e+00	1.56e+00	4.53e-01	4.53e-01	3.51e-02	3.51e-02	9.450-03	2.49-03	4.05e-05	9.92e-06	1.55e-15	1.14e-47	Pred. No.	

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Mouse Chromosome 10 BA	sapiens chromo	sapie	Human PAC clone DJ1139	Drosophila melanogaste	WORKING DRAFT SEQUENCE	Human CYP11B2 gene for	cine max extens	musculus mRNA	musculus gene		Rattus norvegicus amil	D.melanogaster synanto	۵.,	H.sapiens Cyplibl gene		Soybean hydroxyproline	Trypanosoma cruzi mRNA	Sequence 6 from Patent) chromosome 12	sapiens clone	sapiens	sapiens chromoso	PAC clo	ens DNA from	oiens fuc	sapiens mye	otein A	ence 2 from v	histone H4 gene	Human protein A altern
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AL1GNMENTS

	COMMENT	JOURNAL	REFERENCE AUTHORS T1TLE	AUTHORS TITLE JOURNAL REMARK	SOURCE SOURCE ORGANISM REFERENCE	RESULT 1 LOCUS DEFINITION ACCESSION NID VERSION
Sequence Quality Assessment: This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than	BOX 352143 Seattle, WA 98195 Contact: Daniel E Geraghty (geraghty@fhcrc.org) Overlapping Sequences: 5': UWGC:370m33.013 (Genbank Accession: AC005530) 3': UWGC:y67c112 (Genbank Accession: AC004211)	Submitted (05-NOV-1998) Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA University of Washington Human Genome Center	The Clinical Research Division 1100 Fairview Ave. N., P.O. Box 19024 Seattle, WA 98109-1024 2 (bases 1 to 47323) Geraphty, D.E. and Olson, M.V. Direct Submission	Janer,M., Guillaudeux,T., Vu,Q., Kutyavin,T., Harter,H. and Geraghty,D.E. Large scale sequence analysis of the human MHC class I region Unpublished (1998) Fred Hutchinson Cancer Research Center	HTG. human. human. HOMO sapiens EUKARYOta; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; HOminidae; HOMO. 1 (bases 1 to 4723)	AC005937 47323 bp DNA PRI 05-NOV-1998 HOmo sapiens clone UWGC:370M23.002 from 6p21, complete sequence. AC005937 93845393 AC005937.1 GI:3845393

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This sequence has been validated by Multiple Complete Digest Mapping. Comparison of the experimentally derived map digest fragments with sequence-predicted fragments is given below.

Small fragments below a variable cutoff (approximately 400-600bp) are not mapped and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragment groups are separated by dashed lines.
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Base-by-base quality values are not generally visible from the Genhank flat file format but are available as part of this entry's ASN.1 file.
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25510. .2
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7286. .7584
                                          /rpt_family="MER20" 31295. .31594
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/rpt_family-"Alu"
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Best Local Similarity 100.0%;
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            35465 CAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCT 35524
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                                                                                                                                                                                                                                                    I66494 7218 bp
Sequence 14 from patent
I66494
                                                                                                                                                                                                                         92724471
166494.1
                                                                            Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
Location/Qualifiers
                                                                                                                                                                             Unknown
                                                                                                                           1 (bases 1 to 7218)
Dorner, F., Scheiflinger, F. and Falkner, F. Gunter
                                                                                                                                                            Unclassified.
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/note="clonal variation with 3' overlapping clone insertion of 17bp repeat"
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1491 c 1486 g
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                                     368 others
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FEATURES

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KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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Best Local Similarity 17.9%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (24-JUL-1998) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA (1998 this sequence version replaced gi.3241936. Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA e-mail address: humgen@tigr.org. The orientation of the sequence is from SP6 end to T7 end. Genes were identified by a combination of five methods including: XGRAIL (available by anonymous ftp from
                                                                                                                                                                                                                                                  complete sequence against a peptide database, and the Human gene Index database at TIGR (http://www.tigr.org/cdb/hgi/hgi.html). Genes without pepetide homolgy having spliced EST hits are termed 'Unknown gene product'. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
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1 (bases 1 to 216021)
Adams, M.D., Loftus, B.J., Zhou, L., Crosby, M., Fuhrmann, J.,
Adams, M.D., Loftus, B.J., Zhou, L., Crosby, M., Fuhrmann, J.,
Mason, T.M., Brandon, R., Kim, U.J., Kerlavage, A.R. and Venter, J.C.
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-952F10
                                                                                                                                                                                                                                                                                                                                                                                           arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.Edu/-chris/GENSCANW.html)searches of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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Adams, M.D. and Loftus, B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-JUN-1998) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA, Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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Primates; Catarrhini; Hominidae; Homo.
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AC004787.1 GI:3337381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bjloftus@tigr.org
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Adams, M.D. and Loftus, B.J.
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Pred. No. 9.92e-06;
53; Mismatches 33; Indels 1;
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Best Local Similarity 12.0%;
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Local Similarity 15.1%;
hes 26; Conservative
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                     AR024229
Sequence 22 f
AR024229
93977523
AR024229.1
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Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.
Plant inhibitors of fungal polygalacturonases and
control fungal disease
Patent: US 559830-A 5 29-OCT-1996;
1. .215
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8 c 25 g
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175801. .175945
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Pred. No. 4.05e-05;
51; Mismatches 30;
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US 5569830.
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Best Local Similarity 16.3%;
Matches 26; Conservative
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                                                                                                                                             148 CTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAA 197
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                                                                                                                                                                                                                               18 CNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSANYNYGGNNVGAAK 77
                                                                                                                                                                       78 THYYTHTNVSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSYGSSKTAM 127
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sequence.
AC004787
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128278.1
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Recombinant human anti-Lewis b antibodies

Retent: US 5799961-A 22 18-AUG-1998;

Location/Qualifiers

1. 965
                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 215)
Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use to
                                                                       Homo sapiens Chromosome
                                                                                    HUAC004787 216021 bp
                                                                                                                                                                                                                                                                                                                                                                           Control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
Location/Qualifiers
1. 215
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Unclassified
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Wallace,T_Paul, Harris,W.J., Carr,F.J., Old,L.J.,
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170 c 226 g
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              GI:3337381
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Pred. No. 3.51e-02
42; Mismatches 4
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Pred. No. 9.45e-03;
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                                                                    DNA PRI 24-JUL-1998
16 BAC clone CIT987SK-A-952F10, compl
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30-OCT-1996

JOURNAL FEATURES

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Matches

REFERENCE AUTHORS TITLE

KEYWORDS SOURCE

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                                            1517 YMRGRARKTYYYMARRRGCARSYK-KYMAMYWAAWTTWCAAAAMAAMYTTYYWMMWYYKK 1575
                                                                                                                1457 KKYMWKSMRRARRGSAGKKKKKYYYYYYYYYYYYYYYCMGRAMMAAAWYYKRRSCMAWYY 1516
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           167 GGAGGAATTTGTCAGAAAAGACTCCTTCAGCTTCAGTTGCAAAGTCATACCCGGCCCTGT 108
                                                                               227 TGAAGGGAGATGGAGGAGGAGGCAGAGCTTTCCAAGCAATTCCAGGAAGCTGGACTCATA 168
                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (24-7UI-1998) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
On Jul 24, 1998 this sequence version replaced gi:3241936.
On Jul 24, 1998 this sequence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA e-mail address: humgen@tigr.org. The orientation of the sequence is from Sp6 end to T7 end. Genes were identified by a combination of five methods including: XGRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.Edu/-chris/GENSCANW.html)searches of the complete sequence against a peptide database, and the Human gene index database at TIGR (http://www.tigr.org/tdb/hgi/hgi.html).

Genes without pepetide homolgy having spliced EST hits are termed 'Unknown gene product'. Genes encoding tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE).

Location/qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams,M.D., Loftus,B.J., Zhou,L., Crosby,M., Fuhrmann,J., Mason,T.M., Brandon,R., Kim,U.J., Kerlavage,A.R. and Venter,J.C. Homo sapiens Chromosome 16 BAC clone CIT987SK-A-952F10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 216021)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (bases 1 to 216021)
Adams, M.D. and Loftus, B.J.
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larity 13.8%;
Conservative
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/db_xref="dbSTS:G09935"
199463...199572
/note="on"
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27765. .27872
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/db_xref="taxon:9606"
/chromosome="16"
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/db_xref="dbSTS:G04338"
51778 c 49172 g 53987 t
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/note="16084, CHLC.GCT10B02, Chr. -,

/db_xref="dbsTS:G09703"

175810. .175945
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                                                                                                                                                    Score 27; DB 31;
Pred. No. 3.51e-02;
63; Mismatches 48
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KIAA0304.
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                                                                                                                                                                                                                                                                                                    g2224548
                                                                                                                                                                                                                                                                                                                                                          AB002302
(sites)
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400 GGRTCYGTYTTYCTYRTYTCYCABYTGTTTACCYTCTMBMCYMGSMDGYAYGDGACRDYR 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :|:: : |:| : |:: : |:|:|
114 CCGGGTA-TGACTTTGCAACTGAAGCTG 140
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MORINAGA.T., Chayama,K., Kumada,H. and Ichikawa,Y.

NUCLEIC ACID FRAGMENT WITHIN ENVELOPE REGION OF HEPATITIS C VIRUS
AND METHOD FOR DETECTING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent: JP 1992349885-A 1 04-DEC-1992;
TEIJIN LTD
Direct Submission
Submitted (28-MAR-1997) to the DDBJ/EMBL/GenBank databases. Nobuo Nomura, Kazusa DNA Research Institute, Gene Structure 1; 1532-3 Yana, Kisarazu, Chiba 292, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp, Tel:+81-438-52-3930, Fax:+81-438-52-3931)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepatitis C-like viruses.
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Hepatitis C virus
                                                                                                                                    l (bases 1 to 6252)
Nagase, T., Ishikawa, K.,
Miyajima, N., Kotani, H.,
                                                                                                                                                                                              Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                        Homo sapiens male brain plus clone: HG0016.
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     c12N15/10,C12Q1/68,C12Q1/70//C12N15/11;
strandedness: Single;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus
JF 1992349885-A/1
04-DEC-1992
29-MAY-1991 JP 1991152169
MORINAGA TSUTAE, CHAYAMA KAZUAKI, KUMADA HIROMITSU,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.7%;
larity 34.1%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Hepatitis C virus"
/db_xref="taxon:11103"
-93 c 107 g 85 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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for KIAA0304
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envelope
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Pred. No. 4.53e-01;
29; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA PAT 29-SEP-1997 region of type C hepatitis virus.
                                                                                                                                         Seki, N., Nakajima, D., Ohira, M., Nomura, N. and Ohara, O.
                                                                                                                                                                                                                                                                                                cDNA to mRNA, clone_lib:pBluescriptII
                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                 gene,
                                                                                                                                                                                                                                                                                                                                                                                                                 complete
                                                                                                                                                                                                             Homo.
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                                                                                                                                                                                                                                      Eutheria;
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ACCESSION
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ORIGIN
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Best Local Similarity 78.8%;
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MEDLINE
                     ORGANISM
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                                                                                                                                         11
                                                                           Sequence 1 from 1
A62989
g3716861
                     unidentified
                                                                                                                          A62989
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      unclassified
                                 unidentified
                                                               A62989.1 GI:3716861
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2028 c 1860 g 1204 t
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RFFHLKKTSKEAVGVYRSA1HGRGLFCKRNIDAGEMVIEYSGIVIRSVLTDKREKFYD
GKGIGCYMFRAMDFDVDATMHGNAARFINHSCEPNCFSRVIHVEGQKHIVIFALRRI
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SVHSFMEDMVGILMRHSEEGETPDRRAGGQMKGLLLKLLESAFGWFDAHDFKYWRRST
RLPMGVLLMAVLPPSLDHVYAQWRQQEPETPESGQPPGDPSAAFQGKDPAAFSHLEDP
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DNNYESKWMQCAQCDHWVHAKCEGLSDEDYEILSGLPDSVLYTCGPCAGAAQPRWREA
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/translation-"MGGLSVLTSVPGGPPMVCLLCASKGLHELVFCQVCCDPFHPFCL/translation-"MGGLSVLTSVPGGRKGRGSKHLLECERCRHXYHPACLGPSYPTRA
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1343. .5937
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/db_xref="PID:d1021600"
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/sex="male"
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/db_xref-"taxon:9606"
/clone="HG0016"
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1343. .5932
                                                                                                         60 bp DNA
n Patent WO9720068
                                                                                                                                                                                                                                          Pred.
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Pred. No. 4.53e-01;
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KEYWORDS
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RESULT 13
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                                                                                                                                                                                              670 MVRGK 674
                                                                                                                                                                                                                        130 TGCAAAGTCATACCCGGCCCTGTTCCATGTGAGCTGCCAAGGAGGGTCAAGAGGAGGACA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 CCCTGAAGGGAGATGGAGGAGGAGGCAGAG 201
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                                                           MYU87256 1056 bp DNA
Mustela vison GT dinucleotide repeat,
U87256
                                U87256.1
American mink
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (27-JAN-1997) Breeding and Genetics, Danish Institute of Animal Science, Blichersalle K25, Tjele 8830, DK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.

[ (bases 1 to 1056)
Brusgaard,K., Shukri,N.M., Malchenko,S., Koroleva,I. and Lohi,O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OETUM, H. and Seeger, C.
METHOD FOR GENERATING MULTIPLE DOUBLE STRANDED NUCLEIC ACIDS Patent: WO 9720068-A 1 05-JUN-1997;
BOEHRINGER MANHEIM GME, (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mustela vison
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U87256
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Similarity 10.0%;
3; Conservative
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complement(300. .320)
/standard_name="1167R"
221 c 210 g 2
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gaggatCttaccgctgttgag"
98. 119
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/db_xref="taxon:32644"
a 30 c 0 g
                              GI:4099442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mustela vison"
/db_xref="taxon:9667"
/chromosome="1"
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n GT dinucleotide repeat, chromosome
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Pred. No. 1.
40; Mismatc
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Pred. No. 1.56e+00;
24; Mismatches 3
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ches 17;
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REFERENCE AUTHORS TITLE

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FEATURES

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BASE COUNT
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Carnivora; Pissipedia; Mustelidae; Mustela.
1 (bases 1 to 1056)
Brusgaard,K., Shukri,N.M., Malchenko,S., Koroleva,I. and Lohi,O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g1208739
U47925.1
                                                                                                                                                                                                                                                                                                                                               Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1514)
Ansari-Lari,M.A., Muzny,D.M., Lu,J., Lu,F., Lilley,C.E., Spanos,S. Malley,T. and Gibbs,R.A.
A gene-rich cluster between the CD4 and triosephosphate isomerase genes at human chromosome 12p13
Genome Res. 6 (4), 314-326 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human protein
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                                                                                                                                                                                                                                     Submitted (01-FEB-1996) M. Ali Ansari-Lari, Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston,
                                                                                                                                                                                                                                                                             Ansari-Lari, M.A., Muzny, D.M. and Gibbs, R.A. Direct Submission
                                                                                                                                                                                                                                                                                                                                   96303695
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complement(300. .320)
/standard_name="1167R"
a 221 c 210 g 2:
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Accession Number T99310"
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gaggatcttaccgctgttgag"
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/db_xref="taxon:9667"
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A alternatively spliced form i (A-1) mRNA, complete
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Submitted (12-OCT-1988) Schuemperli D., Zoologisches Institut, Abt.
Entwicklungsbiologie, Baltzerstr. 4, CH-3012 Bern, Schweiz
2 (bases 342 to 1241)
                                                                                                                                             Meier, V.S., Bohni, R. and Schumperli, D
Nucleotide sequence of two mouse hist
Nucleic Acids Res. 17 (2), 795 (1989)
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1678)
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LLPGRHMLFPPLERVHYLQVPLSRRLSHDETNIFSTPREPGSFLHKWSSDDIRVLPA
QSRALGGPPEYLQQRHRLEDDEEDEAEGGGLASLKQFLESGVLGSGGPPRGPGFFR
EEITTFIDETPLSTTASPGHSPRRPPLGLSPRRLSLGSPESRAVGLPLGLSAGRRC
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/db_xref="GI:1208740"
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promoter /clone="53"
/clone="55". 563
/note="pot. 5pl binding site"
/note="Apt. 5pl binding site
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                                                                                                                                                                                                                                                             Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51737-5-4 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q51746 standard;
Q51746;
N81164;
08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutic
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                    New oligo:nucleotide probes specific for Mycobacteria detection and amplification of Mycobacteria nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                   (BECT) BECTON DICKINSON Shank DD, Spears PA; WPI; 93-378844/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide probe MK14-A Oligonucleotide; DNA probe;
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24-MAY-1993; 108325
                                                                         N81164 standard; DNA:
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                                                                                                                                                                    11 ssvhsyyvvhvvshhhsvhhvvhhvhvsvvvhhvvhvvhhvhyhvyvsv 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gagtccagcttcctggaattgcttgaaaagctctgcctcctcctcctccatctcccttcaggg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGGGGTCTGGGCTGCCCTTGTCCTCCTTGACCCTCCTTGGCAGCTCACATGGAACA 110
                                                                                                                                       GCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCTCCACCATGCA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 100.0%;
1 Similarity 100.0%;
234; Conservative
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                                                                                                                                                                                                    Conservative
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                                                                             204
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                                                                             ВP
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Pred. No. 5.37e-133;
Nismatches 0;
                                                                                                                                                                                                  Score 40; D
Pred. No. 9.
45; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mycobacteria;
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                                                                                                                                                                                                                 DB 9; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease diagnosis;
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                substitutions;
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Introducing random point mutations into nucleic acods -
pr by prepn of single Stranded template, annealing a primer, elongation,
pr misincorporation, completion of molecules and screening.
PS Disclosure; p; English.

CC Random point mutations were introduced into the alpha fragment of
CC Encoli beta-galactosidase. The wild type sequence was obtained as a
CC single stranded template and an oligonucleotide was hybridised to
CC it to generate a popn of DNA molecules which terminate at all
CC possible nucleotide positions within a specified region. The
CC variable 3' ends generated in this way are used as primers for
CC reverse transcriptase. Nucleotides are misincorporated by the
CC camplified and then expressed in a suitable host-vector system.
CC amplified and then expressed in a suitable host-vector system.
CC The sequence covers all 176 difft base substitutions, most of which
CC See also P80575.
SQ Sequence 204 BP; 21 A; 47 C; 17 G; 11 T; 108 Others;
                                                                                                             RESULTANT RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 င္ပ
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Query Match
Best Local S
Matches
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Best Local (
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30-MAR-1988; 105163.
03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAY-1993; 108325.
24-MAY-1993; 108325.
24-WAY-1992; US-889651.
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                                                                                                       Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide;
                                                                                                                                                                                                                                                                                                                                 New oligo:nucleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
EP-571911-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAY-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 CCTGTTCCATGTGAGCTGCCAAGGAGGGTCAAGAGGAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 TCATAGGAGGAATTTGTCAGAAAAGACTCCTTCAGCTTCAGTTGCAAAGTCATACCCGGC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 hnhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvhc 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 ymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynv 145
                           Similarity
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.ide probe MK14-A
.ide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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19..69
/*tag= a
/function=multiple cloning site
187..204
/*tag= b
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                        15.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91
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Pred. No. 4.31e-08
54; Mismatches 3;
                        Score 35; DB 9;
Pred. No. 5.35e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bamford J, Reinikainen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39;
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                                                         Length
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Mismatches

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Indels

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Query Match
Best Local s
Matches
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Random point mutations were introduced into the alpha fragment of E. coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAY-1988.
30-MAR-1988;
03-APR-1987;
                                                                                                                                                                                                                                                          77 6
070467 standard; DNA; 114 BP.
070467;
05-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vo-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitution
Escherichia coli.
                                                                                                                                                                        Generic DNA sequence to generate a random TSAR petide library. TSAR: totally synthetic affinity reagent; synthetic; binding ceffector domain; concateneated heterofunctional protein; linke direct; rapid; detection; screening; treatment; generic; ss.
                  WO9418318-A
                                                                                                                      misc_feature
                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  occurred singularly in any given mutant. See also P80575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Introducing random point mutations into nucleic acods by prepn of single stranded template, annealing a primer misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-1988; 105163.
33-ARR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P. Knowles J. Kolvula A. Bamford J. Reinikainen
WPI; 88-279927/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                169 hrnwayvrhdarrddvh 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 GAAAAGCTCTGCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCTCCACCATGCA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 daaawyccyrrsvkydccynachhddhyvybbbvynvhnhnncncccbnnhvchnvhbnn 168
                                                                                                                                                                                                                                                                                                                                                                                            AGATCTCAACACCATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAAGCTGGACTCATAGGAGGAATTTGTCAGAAAAGACTCCTTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.1%;
llarity 11.7%;
Conservative
                               /*tag= a
/note= "this sequence represents '2'; Z can
/note= of 6, 9 or 12 nucleotides (see
                                                                                                                    Location/Qualifiers 55..60
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                                                                                                                                                                                                                                                                                                                                                                                            27]
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Pred. No. 6.41e-06
40; Mismatches 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 Others;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
PT Identifying proteins or peptide(s) which bind a ligand - by PT Screening a recombinant vector library expressing fusion proteins omprising a binding domain and an effector domain PS Disclosure; Page 35; 259pp; English.

CC 070467 is a generic DNA sequence used to generate random TSAR (Totally CC Synthetic Affinity Reagents) peptides. This generic formula can also be crepresented as follows: X(NNB)16/TGC)(NNB)17 (NNB)16/TGC)(NNB)17 X CC and Y are flanking restriction sites (X is not the same as Y) that are constrained by these generic sequences are shown in 070466-68. CC other specified further. Other generic sequences are shown in C70466-68. CC other specified peptides generated by these generic sequences are shown in CC engrising at least two functional regions - a binding domain with a strength of the strength of 
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01-FBB-1994; U00977.
01-FBB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOwlkes DM, Kay BK;
WPI; 94-279739/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
                                                                                                                                                                                                                                                                                 10-APR-1995 (first entry)
10-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding dop
effector domain; concatenated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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01-F2B-1994; UG0977
01-F2B-1993; US-013-30-DEC-1993; US-176
31-JAN-1994; US-189
(UYNC-) UNIV NORTH (
FOWLKES DM, KAY BK
WPI; 94-279739/34
                                                                                                                                                                                                                                                                                                                                                                                                                         Q70470 standard;
Q70470;
    P-PSDB;
                                                                                                                                                                                                                                                     misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGGTCTGGGCTGCCCTTGTCCTCCTTGACCCTCCTTGGCAGCTCACATGGAACAGG
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:-1993; US-176500.
:-1994; US-189331.
:) UNIV NORTH CAROLINA.
SS DM, KAY BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                          /*tag=
/note-
                                                                                                                                                                                                                                                     Location/Qualifiers 55..60
                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         114 BP.
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Pred. No.
31; Misma
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Matches
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18-AUG-1994; U00977.
01-FEB-1994; U00977.
01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLI
FOWLRES DM, Kay BK;
WPI; 94-279739/34.
P-PSDB; R65154.
Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain bisclosure; Page 35; 255pp; English. Q70468 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)11(TGC)(NNB)6Z(NNB)7(TGC)(NNB)107. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generic DNA séquence to génerate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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/note= "this sequence represents '2'; 2
sequence of 6, 9 or 12 nucleotides (see
comments)"
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Pred. No.
29; Misma
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. 8.13e-04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC comprising at least two functional regions - a binding domain with CC affinity for a ligand and a second effector peptide portion that is CC chemically or biologically active. They may further comprise a linker CC peptide between the 2 domains. The oligonucleotides are also designed so CC that the expressed peptide contains 2 or 4 cysteine residues positioned CC in, or flanking, the unpredicted or variant residues. These residues CC confer some degree of conformational rigidity to the peptides. The TSARS CC compans. comprising a TSAR binding domain can be used in rivo to CC deliver a chemically or biologically active molety, eg. metal ion, CC compans. comprising a TSAR binding domain can be used in rivo to CC deliver a chemically or biologically active molety, eg. metal ion, CC compissions of polyclonal antibodies and therefore circumvent the need CC complex methods of hybridoma formation or in vivo antibody CC complex methods of hybridoma formation or in vivo antibody CC production. The TSARs are easily characterised and have designed activity SQ Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins or comprising a binding domain and an effector domain proteins of comprising a binding domain and an effector domain of the proteins of the prot
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01-FEB-1994; U00977.

01-FEB-1993; US-013416.

30-DEC-1993; US-176500.

31-JAN-1994; US-189331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding do effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; SS.
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Q70472;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYNC-) UNIV NORTH CAROLINA. Fowlkes DM, Kay BK; WPI; 94-279739/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 bnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnnnnnnn
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/note= "encoded by
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Pred. No. 2.65e-03;
31; Mismatches 78;
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BESULT OF THE PROPERTY OF THE 
                                               PT Identifying proteins or peptide(s) which bind a ligand - by processing a binding domain and an effector domain fusion proteins comprising a binding domain and an effector domain proteins comprising a binding domain and an effector domain (C 070465 is a generic DNA sequence used to generate random TSAR (Totally C Synthetic Affinity Reagents) peptides. This generic formula can also be crepresented as follows: X(NNB)6(TCC)(NNB)11Z(NNB)14(TCC)(NNB)3Y. X (C and Y are flanking restriction sites (X is not the same as Y) that are constructed by these generic sequences are shown in 070466-68. C other specified further. Other generic sequences are shown in 070466-68. C other specified peptides generated by these generic sequences are shown in 070466-68. C other specified periods generated by these generic sequences are shown in 070466-68. C other specified periods generated by these generic sequences are shown in 070466-68. C other specified periods generated by these generic sequences are shown in 070466-68. C other specified periods generated by these generic sequences are shown in 070466-68. C other specified periods and a second effector peptide portion that is 070466-68. C other specified periods and an openided period generated by these generic sequences are shown in 070466-68. C other specified periods and an openided so other specified periods and an openided so other specified periods. The oligonucleotides are also designed conformationally or biologically active moiety. General specific target or on the 070466-68. C other specified periods are designed of the periods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed conformation or in vivo antibody sequence of the openides and therefore circumvent the need of production. The TSARs are easily characterised and have designed conformation of the openides of the need of the openides of the openi
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Best Local
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01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV MORTH CAROLINA.
FOWLKES DM. KAY BK;
WPI: 94-279729/34.
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/note= *this sequence represents 'Z'; Z
sequence of 6, 9 or 12 nucleotides (see
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.0%;
11.3%;
           12.0%;
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24;
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       28;
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   DB
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       12;
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Length 114;
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Best Local
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Matches 3; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                            A method for treating airway disease in a subject has been produced, which involves the topical administration of an essentially adenosine free antisense oligonucleotide (ON) to the airway epithelium of the subject. The present sequence is an antisense oligonucleotide specific for the human endothelin-1, targeted at the initiation codon. The method can be used to treat airway diseases such as cystic fibrosis, as thma, chronic obstructive pulmonary diseases, bronchitis and other airway diseases characterised by an inflammatory response. By eliminating adenosine from the antisense ON, its liberation upon antisense degradation is prevented, thereby preventing adenosine-induced bronchoconstriction in patients with hyper-reactive airways. Sequence 178 BP; OA; 52 C; 46 G; 32 T;
                                                                                                            Generic DNA sequence to generate a random TSAR-9 petide library. TSAR: totally synthetic affinity reagent; synthetic; binding dom effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                                                                                                                             Q70466 standard; DNA; 114 BP. Q70466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subject
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Metager WJ, Nyce JW;

WPI, 97-051871/05.

Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of
                                                                        misc_feature
                                                                                                      Synthetic.
                                                                                                                                                                                05-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        numan endothelin-l antisense oligonucleotide.
Asthma; airway epithelium; adenosine free; cystic fibrosis;
chronic obstructive pulmonary disease; bronchitis; ss.
Synthetic.
                                                                                                                                                                                                                                                                         118
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                                                                                                                                                                                                                                                                                                     160
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                                                                                                                                                                                                                                                                                                                                   58
                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
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                                                                                                                                                                                                                                                                                                     gggbtcbbbbbc 171
                                                                                                                                                                                                                                                                                                                                                          cttggcbbgccbcbbbcbgcbgbgbgbbbbtcbtgbgcbbbtbbtccbttctgbbbbbbb 159
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                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               009306
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                /*tag= a
/*tag= a
/note= *this sequence represents 'I';
/note= *this sequence represents 'I';
sequence of 6, 9 or 12 nucleotides (sometimes)
                                                                        Location/Qualifiers 55..60
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                                                                                                                                                                                                                                                                                                                                                                                         Score 28;
Pred. No.
32; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                        DB 32;
2.65e-03;
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                                       can
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WO9418318-A

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CC that are not specified further. Other generic sequences are shown in CC 070466-68. Dther specific peptides generated by these generic sequences

CC are shown in R65151-54. TSARs are concatenated heterofunctional proteins

CC of peptides, comprising at least two functional regions - a binding

CC domain with affinity for a ligand and a second effector peptide portion

CC that is chemically or blologically active. They may further comprise a

CC linker peptide between the 2 domains. The oligonucleotides are also

CC designed so that the expressed peptide contains 2 or 4 cysteine residues

CC positioned in, or flanking, the unpredicted or variant residues. These

CC positioned in, or flanking, the unpredicted or variant residues. These

CC positioned in, or flanking a TSAR binding domain can be used in

CV vivo to deliver a chemically or biologically active moiety, eg. metal

CC ion, radiolasotope, peptide, toxin or enzyme, to the specific target or

CC monoclonal or polyclonal antibodies and therefore circumvent the need for

CC complex methods of hybridoma formation or in vivo antibody production.

CC flee TSARs are easily characterised and have designed activity allowing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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01-FEB-1993: US-013416.
30-DEC-1993: US-176500.
31-JAN-1994: US-189331.
(UYNC-) UNIV NORTH CÁROL.
FOWLKES DM. KAY BK;
WPI: 94-27973/34.
WO9418318-A.
118-AUG-1994.
01-FEB-1994;
01-FEB-1993;
30-DEC-1993;
31-JAN-1994;
(UYNC-) UNIV
Fowlkes DM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying proteins or peptide(s) which bind a ligand screening a recombinant vector library expressing fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; R65152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding do effector domain; concateneated heterofunctional protein; linker direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q70469;
07-APR-1995 (first entry)
Generic DNA sequence to ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-AUG-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 TTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAAATGCTTGAAAAGCTCTGCCT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 bnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnb 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 11.5%;
Local Similarity 4.9%;
nes 5; Conservative
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                                   ; U00977.
; US-013416.
; US-176500.
; US-189331.
V NDRTH CAROLINA.
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/note= "this sequence represents'
sequence of 6,9 or 12 nucleotides
comments)"
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Pred. No.
28; Misma
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PT Identifying proteins or peptide(s) which bind a ligand - by PT Identifying proteins or peptide(s) which bind a ligand - by PT screening a recombinant vector library expressing fusion proteins PT comprising a binding domain and an effector domain PS Disclosure; Page 35; 25pp; English.

PS Disclosure; Page 35; 25pp; Page 35; Page 3
  PR 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                         Fusion protein; ballast constituent, recombinant protein production; HMG CoA reductase; human 3-hydroxy-3-methylglutaryl-coenzyme A-reductase; mixed oligonucleotide; ss.
US5227293-A.
13-JUL-1993.
29-AUG-1989;
29-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 94-279739/34
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                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q51787 standard; DNA;
                                                                                                                                                                                           repeat_unit
                                                                                                                                                                                                                                                                                                                                             repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 TGAAAAGCTCTGCCTCCTCCATCTCCCTTCAGGGACCAGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 GAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCT 193
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  US-399874
                                                                         /rpt_type= tandem /note= "can be repeated z times, where z provided that y+z is 6-12; N stands for identical or different nucleotides, excluding stop codons"
                                                                                                                                                                                                                                                          /rpt_type= tandem /note= "can be repeated y times, where y is 4-11, provided that y+z is 6-12"
                                                                                                                                                                                             /note=
36..38
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Pred. No. 2.70e-
30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
C;
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2.70e-74;
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HE SULT THE 
PT Identifying proteins or peptide(s) which bind a ligand - by PT Identifying proteins or peptide(s) which bind a ligand - by PT Generity a binding domain and an effector domain PS Disclosure; Page 36; 255pp: English.

CC 070470 is a generic DNA sequence used to generate random TSAR (Totally CC Synthetic Affinity Reagents) peptides. This generic formula can also be CC (CAC)2(NNB) RY. X and Y are flanking restriction sites (X is not the same CC as Y) that are not specified further. The peptides generated by this and CC incorporated into variant sequences. TSARs are concatenated conceptorated into variant sequences. TSARs are concatenated conceptorated portion that is chemically or biologically active. They can further comprise a linker peptide between the 2 domains. The TSARs concepts or compsiss. comprising a TSAR binding domain can be used in vivo to CC deliver a chemically or biologically active mote cell. They can also replace the function of macromolecules. Genoculonal or polyclonal antibodies and therefore circumvent the need CC monoclonal or polyclonal antibodies and therefore circumvent the need CC production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
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Matches
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118-AUG-1994
01-FEB-1994; U00977.
01-FEB-1993; US-013415
30-DEC-1993; US-176500.
31-AAN-1994; US-189331
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Claim 9: Column 30: 22pp; English.

Claim 9: Column 30: 22pp; English.

This preferred mixed oligonucleotide encodes a ballast constituent and is inserted between a regulatory region and the structural gene encoding a desired protein, esp. pro-insulin. The short ballast component improves protease resistance of the fusion protein while still allowing the desired protein to adopt its correct conformation prior to cleavage of the ballast constituent.

Sequence 39 Bp; 1 A; 11 C; 1 G;
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Fowlkes DM, Kay BK;
WPI: 94-279739/34.
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070470 standard; DNA; 114 BP.
070470;
070470;
10-APR-1995 (first entry)
10-APR-1995 (first entry)
10-BPR-1995 (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Habermann P, Seed
WPI: 93-235119/29.
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(GEHO ) GEN HOSPITAL CORP.
(FARH ) HOECHST AG.
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/note= "encoded by Z (see comments)"
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Pred. No. 8.42e-02;
20; Mismatches 4
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Matches 8; Conse
                                      144 CCTTCAGCTTCAGTTGCAAAGTCATACCCGGCCCTGTTCCATGTGAGCTGCCAAGGAGGG 85
   84
                        78
                                                         TCAAGAGGAGGACAAGGGGCAGCCCAGACCCCA 52
                    bcacnnbnnbnnbnnbnnbnnbnnbcacca 110
                                                                                  10.7%;
ilarity 8.6%;
Conservative
                                                                                 Score 25;
Pred. No.
23; Misma
                                                                                  Mismatches
                                                                            ; DB 12; Lc.,
b. 8.42e-02;
--hes 62;
                                                                                                    Length 114;
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                                                                                Gaps
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Search completed: Sun Oct 24 18:00:18 1999 Job time: 78 secs.

COllins, Biocomputing Research Unit. Collins, Biocomputing Research Unit. See Search, University of Edinburgh, U.K. rights by Oxford Molecular Ltd see search, using Smith-Waterman algorithm 100:35 1999; MasPar time 20.77 Seconds 974.434 Million cell updates/se 100:35 1999; MasPar time 20.77 Seconds 974.434 Million cell updates/se 100:09092296.seq 100:09092296.	1 48 20.5 7218 c 2 2 12.4 215 c 3 28 12.0 965 c . 4 27 11.5 215 c . 6 23 9.8 2277 c 6 23 9.8 2277 c 7 22 9.4 965 c 110 21 9.0 65 c 111 21 9.0 68 c 112 21 9.0 74 c 114 21 9.0 75 c 115 21 9.0 74 c 116 21 9.0 75 c 117 21 9.0 75 c 118 21 9.0 81 c 119 21 9.0 906	Pred. No. is the number score greater than or e and is derived by analy greater than or e and is derived by analy greater than the score Match Length D	ssued :5A_COM	Nmatch STD: Dbase 0; Searched: 165359 seq Post-processing: Minimum Ma	Title: >US-09-092-2 Description: (51-284) fro Perfect Score: 234 N.A. Sequence: 51 ATGGG Comp: TABLE defaul . Gap 6	Release 3.1A John F. Copyright (c) 1993-1 Distribution MPsrch_nn n.a n.a. databa Run on: Sun Oct 24 18 Tabular output not generated.	
######################################	US-08-232 Sequence US-08-238 Sequence US-08-38 Sequence US-08-38 Sequence US-08-676 Sequence US-08-676 Sequence PCT-US95-1 Sequence US-08-471 Sequence PCT-US95-1 Sequence	of results predicted qual to the score of t sis of the total score SUMMARIES B 1D Descrip	2:5B_COMB 3:5C_COMB 4: Variance 4.241; scal	ry 0 43243793 bases x 0%. 45 summaries	-296-7 rom US09092296.seq GGGTCTGGGCTGCCT CCCAGACCCGACGGGGA	Collins, Biocompub98 University of pights by oxford rights by oxford sae search, using 100:35 1999; Masp 974.	
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PRICATION NUMBER: U FILING DATE: APPLICATION NUMBER: U FILING DATE: APPLICATION NUMBER: E FILING DATE: 26-AUG-1 ATTORNEY/AGENT INFORMATI NAME: BENT, Stephen A REGISTRATION NUMBER: REFERENCE/DOCKET NUMB TELECOMMUNICATION INFORM TELECOMMUNICATION INFORM TELECAM: (703)683-410 TELEZAX: 899149	0299 0299 BLE FORM Floppy FM PC con STEM: PC STEM: PC ATION DA: ATION DA: NUMBER: ON: 435	uence 14, Application US/ uence 14, Application US/ int No. 5670367 BERAL INFORMATION: REPALICANT: DORNER, F. RPPLICANT: SCHEIFLINGER, RPPLICANT: FALKNER, F. G. VITLE OF INVENTION: RECOIUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS: ADDRESSEE: Foley & Lard STRREET: 1800 Diagonal I CITY: Alexandria STATE: VA COUNTRY: USA COUNTRY: USA	STANDARD			5235 5235		909 909 909	800 800 800 800 800	806 906 906 906
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Query Match
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SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER
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Sequence 5, Application US/08238163
Patent No. 5569830
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pT3pt-F1s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: BENNET
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 CTGCCCCTTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATG 122
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LoCal Similarity 1.8%; Pred. No. 3.43e-17;
nes 4; Conservative 130; Mismatches 86; Indels
                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATION
COMPATION
COMPUTER: IBM PC COMPATION
COMPUTER: IBM 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LABAVITCH, John M. APPLICANT: POWELL, Ann APPLICANT: STOTZ, Henrik
                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,16
                                                                                                                                                REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                        FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: BASTLAN, KEVIN L.
REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACA 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 94105-1493
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STOTZ, Henrik
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             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/08388672A Sequence 22, Application US/08388672A
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           MOLECULE TYPE: DNA (genomic)
SEQUENCE 965 BP; 192 A; 170 C; 226 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 -GSSKTAMTSRNRTGKTANNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 GAC-TCATAGGAGGAATTTGTCAGAAAAGACTCCTTCAGCTTCAGTTGCAAAGTCATACC 117
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 1.215
OTHER INFORMATION: /star
OTHER INFORMATION: seque
                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: HADSON, NO. 5795961man D
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YSSANYNYGGNNYGAAKTHYYTHTNYSGADSKTYTDSYNASGTSSSNGGTDGNRSGADSY 120
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Local Similarity 15.1%; Pred. No. 2.36e-05;
hes 26; Conservative 69; Mismatches 75; Indels
                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MINVINSSSSVVSRTASCNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNK 60
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 965 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Carr, Frank J.
APPLICANT: Old, Lloyd J.
APPLICANT: Welt, Sydney
APPLICANT: Kitamura, Kunio
                                    MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Recombinant Human Anti-Lewis
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                                                                                                                                                           TELEPHONE: 212-838-3884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
                                                      TOPOLOGY:
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                                                                     STRANDEDNESS:
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Harris, William J
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Query Match
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Best Local
                                                     LOCATION: 1..215
OTHER INFORMATION: /standard_name= "Deduced amino acid OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application Sequence 5, Application Patent No. 5569830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-238-163-5 STANDARD;
                                                                                                                                                                                                                              TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 771 AARTGGGTKKGURHUYHYSGGYRSTSTCTASDYTTSYWGWYRGRGWGDYGGGYYNYNGKR 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 CATGTGAGCTGCCAAGGAGGGTCAAGAGGAGGACAAGGGG 66
                                                                                                                                 MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: POWELL, Ann
APPLICANT: STOTZ, HENRIK
TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THE
CORRESPONDENCES: 24
CORRESPONDENCES ADDRESS:
                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BENNETT, Alan
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                 NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGAATTTGTCAGAAAAGACTCCTTCAGCTTCAGTTGCAAAGTCATACCCGGCCCTGTTC 106
                                                                                                               NAME/KEY: misc_feature
                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                NAME: Bastian,
                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 03-MAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
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       Similarity
22; Conser
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      Conservative
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                                                                                                                                                                                               215 base pairs
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                                                                                                                                                           unknown
                                                                                                                                            protein
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                  11.5%;
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US/08238163
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Pred. No.
65; Misma
   Score 27; DB 1; L
Pred. No. 3.38e-04;
42; Mismatches 45
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   45; Indels
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                            Length 215;
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                                                  Sequence 2, Application Sequence 2, Application Patent No. 5770422
                                                                                                                     US-08-676-974-2 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA SEQUENCE 2277 BP; 511 A; 212 C; 395 G; 216 T; 943 OTHER.
                                                                                                            XXXXXX
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                                      GENERAL INFORMATION:
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                                                                                                                                                                          224 AGGGAGATGGAGGAGGGAGGCTTTTCAAGCAATTCCAGGAA 180
                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 CTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAA 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 THYYTHTNYSGADSKTYTDSYNASGTSSSNGGTDGNRSGADSYGSSKTAM 127
NUMBER OF SEQUENCES:
             APPLICANT: COLLINS, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415)343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law
STREET: 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: COLLINS, KATHLE TITLE OF INVENTION: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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STATE: C
COUNTRY:
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Similarity 40.0%;
18; Conservative
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(415)363-4342
TD NO: 2:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                        KATHLEEN
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US/08676967
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                                                                                                                                                                                                                                 Score 23; DB 2;
Pred. No. 5.68e-02
13; Mismatches 1
          Telomerase
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                                                                                                                      2277
                                                                                                                      ВP
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                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                           Length 2277;
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Matches

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Best Local S
Matches 1
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NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36.627
REFERENCE/DOCKET NUMBER: UCB96-055
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415)343-4341
TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                    Sequence 99, Application PC/TUS9511934
Sequence 99, Application PC/TUS9511934
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1036 WSNGARGARGARYTNGGNGARYTNYTNCARCARTTYGGNGAR 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: cDNA
SEQUENCE 2277 BP; 511 A; 212 C; 395 G; 216 T; 943 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                      PCT-US95-11934-99 STANDARD; DNA; UNC; 75
                                                                                                                                                                                                                                                                                                                                                                                                                                     224 AGGGAGATGGAGGAGGCAGAGCTTTTCAAGCAATTCCAGGAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 9.8%;
Local Similarity 40.0%;
les 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTT Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                  APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DCCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/11934
                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 200 LL CITY: San Francisco
                                                                                                                                                                               COUNTRY: US
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/676,974 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
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                                                              FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                      New York
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                                                                           20-SEP-1995
                       18,872
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Pred. No. 5.68e-02
             1101-196-228
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                                              Matches
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Best Local Similarity 8.7%;
Query Match 9.4%;
Best Local Similarity 8.7%;
Matches 6; Conservative
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Sequence 97, Application PC/TUS9511934
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic) SEQUENCE 75 BP; 1 A; 1 C; 7 G; 5 T; 61 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US95-11934-97 STANDARD; DNA; UNC; 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 6514 PENNIE
INFORMATION FOR SEQ ID NO: 99:
                                                MOLECULE TYPE: DNA (genomic)
SEQUENCE 82 BP; 1 A; 2 C; 10 G; 8 T; 61 OTHER.
                                                                                                                               TELEX: 66141 PENNIE INFORMATION FOR SEO ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 CCCCCTATG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 NBGGTTGTG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 GGGTCTGGGCTGCCCCTTGTCCTCCTTGACCCTCCTTGGCAGCTCACATGGAACAGGG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
LENGTH: 75 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Antigen Binding PTITLE OF INVENTION: Peptide Libraries NUMBER OF SEQUENCES: 103
                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cytogen Corporation
                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 82 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 20-SEI CLASSTFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Li
                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
                                                                                           TYPE: nucleic acid
                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                        TOPOLOGY:
                                                                                STRANDEDNESS: single
                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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1155 Avenue of the Americas
                                                                                                                                                        (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                               USA
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Pred. No. 1.95e-(
                                                                                                                                                                                                        18,872
Score 22: DB 4; Length 82; Pred. No. 1.95e-01; 19; Mismatches 44; Indels
                                                                                                                                                                                            1101-196-228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptides (Abtides) From
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114 CCGGGTATG 122 72 NBGGTTGTG

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Patent No.

GENERAL

INFORMATION:

APPLICANT: Wallace, T. Paul APPLICANT: Harris, William J. APPLICANT: Carr, Frank J. APPLICANT: Old, Lloyd J.

APPLICANT:

Kitamura, Kunio Carr, Frank J. Welt, Sydney

CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe and Lynch

STREET:

805

Third Avenue

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COMPTTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
OURBENT APPLICATION DATA: US/08/388,672A
FILING DATE: 14-FEB-1995
CLASSIFICATION: THEODILATION.
   US-08-471-052A-145 STANDARD; DNA; UNC; 65 BP
                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
SEQUENCE 965 BP; 192 A; 170 C; 226 G; 200 T; 177 OTHER.
                                                                              934 SGSGIDYTISSDATYYCGTHARIGGTKVKG 963
                                                                                                                                               874 TVTVSSHUVKDMTSSSSASVGDRVTTCRSSTTHGNGNTYYWYKGKAKYRVSNRSGVSRSG 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/08388672A Sequence 22, Application US/08388672A Patent No. 5795961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-388-672A-22 STANDARD; DNA; UNC; 965 BP
                                                                                                                    52 TGGGGTCTGGGCTGCCCTTGTCCTCCTCTTGACC-CTCCTTGGCAGCTCACATGGAACA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Recombinant Human Anti-Lewis B TITLE OF INVENTION: Antibodies NUMBER OF SEQUENCES: 25
                                                               GGGCCGGGTATGACTTTGCAACTGAAGCTG 140
                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hanson, No. 5795961man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGTCTGGGCTGCCCTTGTCCTCCTTGACCCTCCTTGGCAGCTCACATGGAACAGGG 113
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Best Local Similarity 13.8%;
Matches 9; Conservative
                                                                  Sequence 143, Application US/08471052A
Sequence 143, Application US/08471052A
Patent NO. 562903
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: FOwlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA
SEQUENCE 65 BP; 3 A; 3 C; 3 G; 2 T; 54 OTHER.
                                                                                                                                                                                                        XXXXXX
                                                                                                                                                                                                                  US-08-471-052A-143 STANDARD; DNA; UNC; 68 BP
                                                                                                                                                                                                                                                                                                                                178 CTGGACTCATAGGAGGAATTTGTCAGAAAAGACTCCTTCAGCTTCAGCTTGCAAAGTCATA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 145, Application US/08471052A Sequence 145, Application US/08471052A Patent No. 5625033 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               118 ccccc 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9990
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 145:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/4
FILLING DATE: 06-JUNE-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,87
                                                                                                                                                                                                                                                                                                          61 CCTGG 65
                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 65 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York
COUNTRY: "
ZIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166
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Pred. No. 6.54e-01;
16; Mismatches 40
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CITY: New York
STATE: New York
COUNTRY: U.S.A.

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RESULT ID U

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Matches Query Match Best Local

Local Similarity 20.0%; hes 18; Conservation

TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 965 base pairs

STRANDEDNESS:

unknown

nucleic acid

TELECOMMUNICATION INFORMATION: TELEPHONE: 212-688-9200

ATTORNEY/AGENT INFORMATION: NAME: Hanson, No. 579596

COUNTRY:

U.S.A

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Best Local Similarity 13.8%;
Matches 9; Conservative
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TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 143:

SEQUENCE CHARACTERISTICS: .

LENGTH: 68 bases

TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA

SEQUENCE 68 BP; 3 A; 3 C; 5 G; 3 T; 54 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 94, Application PC/TUS9511934
Sequence 94, Application PC/TUS9511934
GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSOTWARE: PALENTIN PC-DOS/MS-DOS
OSOTWARE: PALENTIN PC-DOS/MS-DOS
OFFICIAL PALENTIN PC-DOS/MS-DOS
OFFICIAL PALENTIN PC-DOS/MS-DOS
OFFICIAL PALENTIN PC-DOS/MS-DOS
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PCT-US95-11934-94 STANDARD; DNA; UNC; 74 BP
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FILING DATE: 06-JUNE-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,72
REFERENCE/DOCKET NUMBER: 1101-179
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
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ZIP: 100
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1155 Avenue of the Americas
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Pred. No. 6.54e-01;
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Best Local 9
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Query Match 9.0%;
Best Local Similarity 13.7%;
Matches 10; Conservative
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TELEFAX: (212) 869-9741.
TELEFAX: (212) 869-9741.
TELEFAX: 6141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic) SEQUENCE 74 BP; 3 A; 4 C; 3 G; 1 T; 63 OTHER.
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Sequence 100, Application PC/TUS9511934
GENERAL INFORMATION:
                                            MOLECULE TYPE: DNA (genomic) SEQUENCE 74 BP; 6 A; 6 C; 1 G; 1
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
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NAME: Misrock, S. Lesile
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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TOPOLOGY: 111
                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 20-SE CLASSIFICATION:
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STATE: New York
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nucleic acid
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Pred. No. 6.54e-01
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  Score 21; DB 4; Length 74; Pred. No. 6.54e-01; 17; Mismatches 46; Indels
                                                1 T; 60 OTHER
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Best Local
Sequence 99, Application PC/TUS9511934 Sequence 99, Application PC/TUS9511934 GENERAL INFORMATION:
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
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РСТ-US95-11934-99 STANDARD; DNA; UNC; 75 ВР.
                                                 XXXXXX
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP; 6 A; 6 C; 1 G; 1 T; 60 OTHER.
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                                                                                                         65 CAGCCCA 59
                                                                                                                                 65 NACCACA 71
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REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 20-SEI CLASSIFICATION:
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STATE: New York
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Conservative
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1155 Avenue of the Americas
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Peptide Libraries
103
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                                                                                                                                                                                                  Score 21; DB 4; Length 74; Pred. No. 6.54e-01; 19; Mismatches 43; Indels
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Search completed: Sun Oct 24 18:00:58 1999 Job time: 23 secs.
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Best Local :
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
TYPE: nuclet acid
STRANDEDNESS: single
                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 75 BP; 1 A; 1 C; 7 G; 5
                                                                                          149 AGACTCCTTCAGCTTCAGTTGCAAAGTCATACCCGGCCCTGTTCCCATGTGAGCTGCCAAG 90
                                                 89 GAGGGT
                                                                        64 NNBGGT 69
                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
                                                                                                                                                       ocal Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHX: (212) 869-9741/8864
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ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Pennie &
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TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
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                                                                                                                                             Conservative
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1155 Avenue of the Americas
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7.6%;
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                                                                                                                                          Score 21; DB 4; Length 75; Pred. No. 6.54e-01; 18; Mismatches 43; Indels
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SUMMARIES Description 10 Description All36523 UI-R-C2P-ng-e-02-0-UI. AA754459 97SN1787 Rice Immature AA754459 97SN1787 Rice Immature AA754458 97SN1784 Rice Immature AA7034173 Human mRNA (T AF034173 Human mRNA (T	Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.	emb1-est58 1:em_est10 2:em_est11 3:em_est17 4:em_est18 5:em_6 6:em_est9 7:em_gss1 genbank-est111 1:gb_est11 11:gb_est12 12:gb 8:gb_est1 9:gb_est15 15:gb_est16 16:gb_est17 13:gb_est14 14:gb_est15 15:gb_est2 20:gb_est20 21:gb_est21 22:gb_est2 23:gb_est2 20:gb_est20 21:gb_est21 22:gb_est2 23:gb_est3 34:gb_est24 25:gb_est25 26:gb_est26 27:gb_est23 24:gb_est28 29:gb_est29 30:gb_est3 31:gb_est4 32:gb_est5 33:gb 34:gb_est7 35:gb_est8 36:gb_est9 37:gb_gss1 38:gb 39:gb_est3 40:gb_gss4 41:gb_gss5 42:gb_gss6	Searched: 2883791 seqs, 1171580779 bases x 2 Post-processing: Minimum Match 0% Listing first 45 summaries	match STD : D	Title: >US-09-092-296-7 Description: (51-284) from US09092296.seq Perfect Score: 234 N.A. Sequence: 51 ATGGGGTTGGGGCTGCCCTACCATGTTGTCTGCAACACA TACCAGACCTGGGACCCGACGACGACCCGACGACCAGACCCGACGACCCGACGA	ohn F. Collins, Biocomputing Research Unit 1993-1998 University of Edinburgh, U.K. bution rights by Oxford Molecular Ltd database search, using Smith-Waterman alg 24 17:50:56 1999; MasPar time 454.93 Sec ated.	
Pred. No. 7.25e.84 2.49e.56 2.28e.30 2.20e.18 2.20e.18 2.20e.17 4.09e.10 4.09e.10 4.10e.09 1.51e.07	rinted,	_est2 b_est13 b_est6 _gss2			JAACACA 284	 Orithm Sonds	(MT)

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AA428548 AQ201160		AA620971	H41536	W07189		B12587			AQ235722			C28493	W79098	W13114		AA730403	W84051	D40392	в81136				AI086444		T15255		AI554565	R52894	W33870	B04965	T52782
7d06.rl Soares_ Ill-46Kl8.TJ RF	CM5G7T7 My h16f01.s1	8f08.sl Soares	71c01.s1 Spares	MIAIII/ SUDERACTED	39H122 normalize	011-Sp6 1 IGF Arab	GH02423.5prime GH Dros	em.est.742 Poplar	2015 B2 C08 T7 C	TC01459 Trypanosom	6f12.v1 Gm-c1004	Rice callus	5hl0 rl Soares	Soares mou	8 Lambda-PRL2 Ara	2c07 s1 NCT CGA	6ell.rl Soares mou	S2342A Rice shoot	T-HSP-2015F16.TFC (R-C3-sw-e-12-0-UI	O Human mRNA /	la08.x1 NCI CGAP B	Se01.x1 NCI CGAP B	OBhO4.rl Spares mon	S855 lambdaZAPST	8b09.rl Soares pin	5f06.x1 NCI CGAF	01d09.rl Soares	c56b03.rl Soares mo	-51A6-11 CSRL f	79f01.rl strata
8.54e-03 8.54e-03	.54e-	.54e-(546	540	.54e-	. 28e-	. 28e-	280	280	200	286	280	280	286	286	286	286	. 28e	286	286	200	220	226		200	200	220	220	220	210	510

ALIGNMENTS

FEATURES	JOURNAL MEDLINE COMMENT	REFERENCE AUTHORS TITLE	NID VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 LOCUS DEFINITION ACCESSION
Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: msoarces@blue.weeg.ulowa.edu The sequence tag present in the cDNA between the NotI site and the coligo-Gr track Served to identify it as a clone from the normalized adult Lung Library.cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics Seq primer: M13 Forward. Location/Qualifiers	On Jan 14, 1998 this sequence version replaced gi:1877567.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 328) Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene	93637300 93637300 EST. Norway rat. Rattus norvegicus	AI136523 328 bp mRNA EST 11-FEB-1999 UI-R-C2p-ng-e-02-0-UI.sl UI-R-C2p Rattus norvegicus cDNA clone UI-R-C2p-ng-e-02-0-UI 3', mRNA sequence.

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116; Conser
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AA754459
                                                     Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
On Jan 14, 1998 this sequence version rankaged citylogical controls.
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97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
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Nahm, B. H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P.

Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.,

Lee, M.C. and Eun, M.Y.
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Contact: Eun M.Y
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/note="Vector: pTTT3D-Pac (Pharmacia) with a modified
/note="Vector: pTTT3D-Pac (Pharmacia) with a modified
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library is a subtracted library derived from the UI-R-C1
library which is a subtracted library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung brain, liver,
kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
embryo: The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which allows
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Best Local Similarity 10.9%; Pred. No. 2.49e-56;
Matches 23; Conservative 108; Mismatches 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 CAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAA 188
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Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun8sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449 728 bhnahm@bioserver.myongji.seq primer: M13 Reverse Primer.
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Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,

Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,

Lee,M.C. and Eun,M.Y.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
      Department of Cytogenetics
National Inst. of Agri. Sci.
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
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On Jan 14, 1998 this sequence version replaced gi:1797457.
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21 c 12 g 35 t 179 others
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20-JAN-1998

Length 252

2: Gaps

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                                                      Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Back Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea, 449-728 bhnahm@bioserver.myongji.seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                      Nahm, B.H., Kim, J.K., Cheong, J. Kim, W.T., Kim, W.Y., Yang, M.S., Lee, M.C. and Eun, M.Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza.
/organism="Oryza sativa"
                                Location/Qualifiers
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/clone_lib="Rice Immature Seed Lambda
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coll SOLK"
21 c 12 g 35 t 179 oth
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/cultivar="Milyang23"
/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4830"
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10.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
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Pred. No. 2.28e-30;
79; Mismatches 58
                                                                                                                                                                                                                                                                           replaced gi:1797455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 CAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 YYARSKYGYGTBYYSWNVDTNTGGTGVGKTTVNVHSGWNNRCSNSVVYVWBTAYCDYBHY 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ÚП
                                                                                                                                                                                                                                                                                       Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Back Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea, 49-728 bhnahm@bioserver.myongji.seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Eun M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 247)
Nahm, B. H., Kim, J.K., Cheong, J. J., Kim, S. I., Hahn, T. R, Moon, E. P.,
Kim, W. T., Kim, W. Y., Yang, M. S., Park, R. D., Sohn, U. I., Kang, K. Y.,
Lee, M. C. and Eun, M. Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa.
Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Jan 14, 1998 this sequence version replaced gi:1797455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
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llarity 15.48;
Conservative
                                                                    /organism="Oryza sativa"
/cultivar="Milyang23"
/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
                                                         /map="6"
                                                                                                                                                                                                                                            Location/Qualifiers
1. .247
        /clone_lib-"Rice
                                  /clone="97SN1784"
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/dev_Stage="S days after pollination"
/lab_host="B. coli SOLR"
/lab_host="B. coli SOLR"
/lab_host="B. coli SOLR"
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/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI, Distributional cDNA library inserted into lambda ZAPI; Vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
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/clone_lib="Rice Immature Seed Lambda
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Pred. No. 2.20e-18;
55; Mismatches 55
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     Seed
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Lambda ZAPII cDNA Library"
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Best Local Similarity 14.7%;
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Best Local Similarity 11.2%;
Matches 13; Conservative
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                                                                                                                                                                                     1480 RYKRWKRRKGRRKRMTGMYKRMYRAMMAMCAMMACWWYYWKMRGMKKCWKYRKYKKYTS 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 TGTGA--GCTGCCAAGGAGGTCAAGAGGAGGACAAGGGGCAG 63
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                                                                         159
                                                                                                                                                218 ATGGAGGAGGCAGAGCTTTTCAAGCAATTCCAGGAAGCT-GGACTCATAGGAGGAAT 160
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                                                             TTGTCAGAAAAGACTCCTTCAGCTTCAGTTGCAAAGTCATACCCGGCCCTGTTCCA 104
                                                                                                         TYYKSWSRWYWYTTYTYWYCWCCT-SMKSASCAMMRWMGYMGSRSSRSYWGYWGSM 1594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2275)

Tripodis,N. and Ragoussis,J.

Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guys Hospital
7th floor, Guy's Tower, London
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Tripodis, Nikos
Division of Medical and Molecular Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
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AF038250
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                                                                                                                                                                                                                                                                                                                       438
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/lab_host="E. coli SOLR"
16 c 21 g 34 t 169 oth
                                                                                                                                                                                                                                                                                                                   /clone_lib="Human mRNA (Tripodis and Ragoussis)" 619 c 470 g 599 t 149 others
                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="6p21.3"
                                                                                                                                                                                                                                                                                                                                                            /clone="ntcon2 contig"
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Pred. No. 2.20e-18;
71; Mismatches 66
                                                                                                                                                                                                                                            Score 32; D
Pred. No. 5.
  mRNA
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5.89e-17;
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Best Local Similarity 45.6%;
Matches 26; Conservative
                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         432 GKVGGVBGASTCMTHYNCCDCKTCGSAGVTVNHHDWSMAGGAARAGCTTCTCTCGCA 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g2707735
AF034173.1
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Generation of a transcription map in the region immediately centromeric to human MHC across the 6p2l.2-6p2l.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone ntcon9, mRNA sequence. AF038250
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                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2275)

Tripodis,N. and Ragoussis,J.

Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF034173 2275 bp mRNA EST 30-MAR-1998 AF034173 Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA clone ntcon2 contig, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
On Jan 19, 1998 this sequence version replaced g1:2045085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1287)
                                                                                                                           Contact: Tripodis, Nikos
Division of Medical and Molecular Genetics
Guys Hospital
7th floor, Guy's Tower. London ent one
                                                                                                                                                                                                               boundary
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2045115
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: nikos@nki.nl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guys Hospital
7th floor, Guy's Tower, London
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Division of Medical and Molecular Genetics
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                                                                                                             floor, Guy's Tower, London SEl
il: nikos@nki.nl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="6p21.3"
/clone="ntcon9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Human mRNA (Tripodis and Ragoussis)"
219 c 293 g 361 t 65 others
                                                                        Location/Qualifiers
1. .2275
              /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="6p21.3"
/clone="ntcon2 contig"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:2707735
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Pred. No. 4.09e-10;
15; Mismatches 16
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RESULT
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KEYWORDS
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Best Local Similarity
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Best Local Similarity 17.8%;
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
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                                                                                                                                                                            279 TGCAGACAACATGGTGTGAGATCTTGCATGGTGGAGGGTGACGCTGGTCCCTGAAGGGA 220
                                                                                                                                                                                                  125 TGCAGGTAAGGTGGTGGTGGCCCCTTTATGATGAAGGGTGACATTGGTCCCCGGTGAGA 184
                                                                                                              219 GATGGA 214
                                                                                                                                                185 GGTGGA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 AA-CTGAAGCTGAAGGAGTCTTTTCTGA-CAAATTCCTCCTATGAGT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 TIGICCICCICTIGACCCICCTIGGCAGCICACAIGGAACAGGGCCGGGTAIGACITIGC 129
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        T94049 176 bp mRNA EST 24-MAR-1999 ye33f07.rl Stratagene lung (#937210) Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus sp.
Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Institute for Genomic Research 9712, Medical Center Drive, Rockville, Tel: (301)-838-3529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia, Eutherla; Rodentia; Sclurognathi; Muridae; Murinae; Rattus. 1 (bases I to 190)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI010074 190 bp mRNA EST 15-JUN-1998 EST204525 Normalized rat lung, Bento Soares Rattus sp. cDNA clone RIUB338 3' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1998)
On Jan 19, 1998 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Lee,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene Index
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                                                                                                                                                                                                                                                                                                                                                        39
                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Rattus sp."
/note="Organ: lung; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"
                                                                                                                                                                                                                                                                                                                                                /clone_lib="Normalized rat lung, 51 c 59 g 41 t
                                                                                                                                                                                                                                                                                                                                                                                          /map="21q"
/clone="RLUBT38"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10118"
                                                                                                                                                                                                                                                                            11.1%;
69.7%;
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                                                                                                                                                                                                                                                      Score 26; DB 21; LA
Pred. No. 8.11e-09;
0; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 27; DB 20;
Pred. No. 4.09e-10;
53; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      replaced gi:2151091
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                                                                                                                                                                                                                                                                                            Length 190;
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KEYWORDS
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Best Local :
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                                                                                                                                                                                                                                                                                                                                        9654642
T52782.1
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 398)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 176)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. WashU-Merck EST project
Unpublished (1995)
                                                                                                                                                                                                                        ya79f01.rl Stratagene ovary (#937217) Homo sapiens IMAGE:67897 5', mRNA sequence.
                                                                                                  Eukaryota; Metazoa;
                                                                                                                    Homo sapiens
                                                                                                                                                                                                                  T52782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
Insert Size: 196
High quality sequence stops: 155 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 196
Std Error: 0.00
Seq.primer: Ml3RP1
                                                                                                                                          numan
                                                                                                                                                                                                                                                                                                                                                                                                                      25;
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                    10.7%;
Similarity 100.0%;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="72 years"
/lab_host="SOLR cells (kanamycin resistant)"
/lab_doc 39 g 39 t 4 others
                                                                                                                                                                            GI:654642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Stratagene lung (#937210)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/clone="IMAGE:119557"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="GDB:487846"
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                                                                                                                                                                                                                                                                  398 bp
                                                                            Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                Score 25; DB 19
Pred. No. 1.5le-
0; Mismatches
                                                                                                                                                                                                                                                                    mRNA
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1.5le-07;
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WashU-Merck EST Pro
Unpublished (1995)
Other_ESTs: ya79f0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B04965 582 bp DNA GSS 26-JUN-1996 CSRL-51A6-u cSRL flow sorted Chromosome 11 specific cosmid Homo saptens genomic clone cSRL-51A6, genomic survey sequence.
                                                                                                                                                                                        Evans,G.A., Burbee,D., Davies,C., Hahner,L., Oliver,T., Gilbert,M., Jones,D., Ward,T., Gillilan,E., Schagemann,J., Probst,S.., Harris,J., DeFord,J., McFarland,J., Burzinski,K., Khan,M., Kupfer,K. and Garner,H.R. GenOmic Sequence Sampled Map of Chromosome 11 Unpublished (1996)
                                                        McDermott Center for Human Growth and Development University of Texas Southwestern Medical Center At 5323 Harry Hines Blvd, Dallas TX 75235-8591
Tel: 214-648-1600
                                                                                                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
1 (bases 1 to 582)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             B04965.1 GI:1414243
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                        Fax: 214-648-1666
                                                                                                                                                Contact: Evans GA, Shane Probst
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop: 352.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95
                  gevans@utsw.swmed.edu, shane@mcdermott.swmed.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: ovary; Vector: Bluescript SK; Site_1: EcoRI; Site_2: Xhor; Cloned unidirectionally. Primer: Oligo dT. Total ovary tissue, normal, caucasian. Average insert size: 0.8 kb, Uni-ZAP XR Vector; -5' adaptor sequence: 5' GRATTCGGACGAG 3' -3' adaptor sequence: 5' CTCGACTTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="SOLR cells (kanamycin resistant)"
125 c 94 g 82 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:67897"
/clone_11b="Stratagene ovary (#937217)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex-"female"
/dev_stage="49 year old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="GDB:504154"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Project
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Pred. No. 1.51e-07
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 CTGGCATGGTGGCAGGTGACTTTAATCCCAGCACTTGGGATGCAGGGGCAGGGCAGAGCTT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 TT 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            w33870 364 bp mRNA EST 13-MAY-1 mc56b03.rl Soares mouse embryo NbME13.5 14.5 Mus musculus clone IMAGE:352493 5', mRNA sequence.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                             l (bases 1 to 364)
Marra, M., Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Watersten, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: T7
Class: cosmid ends
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BACKWARD: TTCAAACTCAAAAAAGCTCTG
                                                                                                                                                                                                                                                                        Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Porest Park Parkway, Box 8501, St. Louis, NO 63108
                                                                                                                                                                                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
Unpublished (1996)
On May 18, 1995 this sequence version replaced gi:811194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g1315794
W33870.1 GI:1315794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                    MGI:224293
                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse
                                                                                                                           primer: ETPrimer
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                                                                                                         quality sequence stop:
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/note="Vector: sCos-1; Human Chromosome 11 specific cosmid
/noter prepared from flow sorted human Chromosome 11
derived from Chinese Hampster Ovary (CHO) monochromosomal
somatic cell hybrid, J1"
/db_xref-"taxon:9606"
/clone="cSRL-51A6"
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/note="Vector: pT7T3D-Pac (Pharmacia) with
                      /organism="Mus musculus"
/strain="C57BL/6J"
                                                                  1. .364
                                                                                  Location/Qualifiers
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Pred. No. 1.51e-07;
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      modified
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Email: est@watson.wustl.edu
High quality sequence stops: 299
Source: IMAGE Consortium LINL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 397)

Hillier_L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                       Seq primer: M13RP1
High quality seque
                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1995)
On Sep 21, 1992 tl
                                                                                                                                                                                                                                                                 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                              The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yh0ld09.rl Soares infant brain
IMAGE:41873 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOmo sapiens
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Similarity 79.5%;
                                                                                                                                     quality sequence stop: 299.
Location/Qualifiers
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/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="bH10B"
73 c 87 g 104 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M.Fatima Bonaldo. "
/db_xref="taxon:10090"
/clone="IMAGE:352493"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397 bp mRNA EST 18-MAY-1995 Ires infant brain INIB Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                         this sequence version replaced gi:275991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 23; DB 34;
Pred. No. 4.22e-05;
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BASE COUNT

Query Match Best Local :

Matches

REFERENCE AUTHORS

VERSION ACCESSION DEFINITION

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'clone_lib="NCI_CGAP_Brn25'

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Query Match
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Matches 3
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1 (bases 1 to 400)

NCI/MINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTCAP). Tumor Gene Index
Unpublished (1998)

On May 7, 1998 this sequence version replaced gi:3121680.
                                                                                                                                                                                                                                                                                                                                          Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI554565 400 bp mRNA EST 23-MAR-1999 tn25f06.xl NCI_CGAP_BIN25 HOMO Sapiens cDNA clone IMAGE:2168675 similar to TR:Q16664 Q16664 PROTEIN A-1. [1] ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST
                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   ww-bio.lln1.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: M. Bento Soares, Ph.D.,
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Ph.D.
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1. .400
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74 c 100 g 104 t 4 other
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Pred. NO. 4.22e-0
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1 90 2 32 3 29 4 28 5 27 6 7 27 6 9 26 6 9 26 6 11 25 6 11 25	1	Pred. score and i	Database: Database:	Post-processing:	Searched:	ch STD	Title: Description: Perfect Score: N.A. Sequence: Comp: Comp:	MPSrch_nn n.a Run on: Tabular output		*
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ALIGNMENTS

COMMENT	TITLE S JOURNAL S REMARK U	-	F &H	RESULT 1 LOCUS DEFINITION I ACCESSION Z NID VERSION Z VERSION Z KEYWORD5 SOURCE I ORGANISM I
Overlapping Sequences: 5: UWGC:370m23.013 (Genbank Accession: AC004211) 5: UWGC:370m23.013 (Genbank Accession: AC004211) 3: UWGC:370m23.013 (Genbank Accession: AC004211) Sequence Quality Assessment: This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than	Greaghty, J. E. and OISON, M.V. Direct Submitssion Submitted (05-NOV-1998) Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA University of Washington Human Genome Center Box 352145 Seattle, WA 98195 Contact: Daniel E. Geraghty (geraghty@fhorc.org)	Fred Hutchinson Cancer Research Center The Clinical Research Division 1100 Fairview Ave. N. P.O. Box 19024 Seattle, WA 98109-1024 2 (bases 1 to 4733)	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 47323) Janer, M., Guillaudeux, T., Vu,Q., Kutyavin, T., Harter, H. and Geraghty, D. E. Large scale sequence analysis of the human MHC class I region Unpublished (1998)	AC005937 47323 bp DNA PRI 05-NOV-1998 HOMO saplens clone UWGC:370M23.002 from 6p21, complete sequence. AC005937 93845393 AC005937.1 GI:3845393 HTG. HTG. HTG. HOMO Saplens

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This sequence has been validated by Multiple Complete Digest Mapping. Comparison of the experimentally derived map digest fragments with sequence-predicted fragments is given below.
Small fragments below a variable cutoff (approximately 400-600bp) are not mapped and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragment groups are separated by dashed lines.
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DS or two Chemistry coverage:
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ORGANISM
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KEYWORDS
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JOURNAL
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Best Local Similarity 98.9%;
Matches 91; Conservative
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                                                                                                                                                                                                                                         sequence.
AC004787
g3337381
                                                           Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 216021)
Adams,M.D., Loftus,B.J., Zhou,L., Crosby,M., Fuhrmann,J.,
Adams,M.D., Loftus,B.J., Kim,U.J., Kerlavage,A.R. and Venter,J.C.
Mason,T.M., Brandon,R., Kim,U.J., Kerlavage,A.R. and Venter,J.C.
Homo sapiens Chromosome 16 BAC clone CIT987sK-A-952Fl0
                                                                                                                                                                                                                                                                                        HUAC004787 216021 bp DNA PRI 24-JUL-1998
Homo sapiens Chromosome 16 BAC clone CIT9878K-A-952F10, complete
Direct Submission
           2 (bases 1 to 216021)
Adams, M.D. and Loftus, B.J.
                                                                                                                                                   Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
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Pred. No. 8.42e-49;
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Best Local Similarity 11.6%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1454 RGKKKYMWKSMRRARRRGSAGKKKKKYYYYYCYYYYYYYYCMGRAMMAAAWYYKRRSCMA 1513
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                                                                                                                                                                                                                                                                                                                                                                                                              70 ACATGGAACAGGGCCGGGTATGA-CTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAA 128
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Sequence 22
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On Jul 24, 1998 this sequence version replaced gi:3241936.
Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA e-mail address: humgen@tigr.org. The orientation of the sequence is from SP6 end to T7 end. Genes were identified by a combination of five methods including: XGRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, Washington), Genscan (Chris 
                                               ÅR024229.1
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3 (bases 1 to 21
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/db_xref="dbSTS:G04338"
51778 c 49172 g 53987 t 124 others
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199463. .199572
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/map="#16q21-22"
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                                                                                                                                       965 bp DNA from patent US 5795961.
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Recombinant human anti-Lewis b antibodies

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Recombinant human anti-Lewis b antibodies

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Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
                              Unknown.
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Similarity 20.68;
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Wallace, T. Paul, Harris, W.J., Carr, F.J., Old, L.J., Welt, S. and
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Pred. No. 2.26e-03;
90; Mismatches 66
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Pred. No. 5.53e-04
47; Mismatches 3:
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                                                                                                                                                                                                                                                  61 YSSANYNYGGNNVGAAKTHYYTHTNVSGADSKTVTDSYNASGTSSSNGGTD-GNRSGADS 119
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Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use to control fungal disease
Patent: US 559830-A 5 29-OCT-1996;
1. 215
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Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and
control fungal disease
Patent: US 556830-A 5 29-OCT-1996;
Location/Qualifiers
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I28278.1
                                                                      Sequence
AR024229
g3977523
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                            Unknown.
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Similarity 13.8%;
22; Conservative
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Pred. No. 9.06e-03;
42; Mismatches 45
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Local Similarity 20.0%;
nes 18; Conservative
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Kitamura, K.

Kitamura, K.

Recombinant human anti-Lewis b antibodies

Recombinant human anti-Lewis b antibodies

Recombinant human anti-Lewis b antibodies

Patent: US 5795961-A 22 18-AUG-1998;

Patent: US 5795961-A 22 18-AUG-1998;
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Homo sapiens sequence.
AC005369
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Wallace, T. Paul, Harris, W.J., Carr, F.J., Old, L.J., Welt, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 74371)

Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Kadner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M., Rojeski,H., Subramanian,S. and Martin,C.H.

Sequencing of human chromosome 5
                                                                                                                                                                                                                                                                                                3 (bases I to 74371)
3 (bases I to 74371)
Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Rojeski,H., Subramanian,S. and Martin,C.H.
Direct Submission
Submitted (01-AUG-1998) Human Genome Center, DOE Joint Genome Submittute, Lawrence Berkeley National Laboratory, MS 74-157,
                                                                                                                                                                                                                                                   Berkeley, CA 94720, U.S.A. Sequence submitted by: DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Large Scale Sequence Analysis and Comparison Analysis (SCAN) System
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170 c 226 g
                                                                                         /note="LBNL H175"
893. .1030
                                                   /rpt_family-"Alu" 2295. .2438
                 /rpt_family="Alu" 2818. .2859
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Location/Qualifiers
/note="(GT)21"
                                                                                                                            /chromosome=
                                                                                                                                                /clone="
                                                                                                                                                              /map="5q"
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/db_xref="taxon:9606"
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s chromosome
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Pred. No. 3.54e-02;
41; Mismatches 30;
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repeat_region complement(199432022) /rpt_family="Alu" repeat_region 2120221496 /rpt_family="Alu" repeat_region 2173622035 /rpt_family="Alu"	T903. 1988 TPt_family="Alu" 1994. 19945 /note="(GTTY)8" /rpt_type=tandem /rpt_unit=GTTT	/rpt_fam compleme /rpt_fam compleme /rpt_fam compleme /rpt_fam		1372713750 /note="(AC)12" /rpt_type=tandem /rpt_unit=AC 1378314024 /rpt_family="L1" 1417514470 /rpt_family="Alu"	repeat_region 12057, 12085 /note="(A)29" /rpt_type=tandem /rpt_unit-A repeat_region 12365, 12645 /rpt_family="Alu"		\0\ 4\\ \0	repeat_region 4366. 4661 /rpt_family="Alu" repeat_region 53275602 /rpt_family="Alu" repeat_region 6586. 6956 /rpt_family="Ll"	<pre>misc_feature join(32463410,37213828) /*standard_name="RLF" /note="65% & 69% protein identity GenPept:U22377" repeat_region</pre>
c_feature cc c_feature cc	Alu" Alu" Jentity EST ou55c09.x1" ST:AI025011*	.33785) .34144) ellent exon, .35331)	misc_feature complement(32159. 32232) /note="GRAIL 2 excellent exon, frame 2" repeat_region 32388. 32488 /pt_family="MLT1" repeat_region 32617. 32908 /rpt_family="Alu" repeat_region 3297. 33088 /rpt_family="MLT1"	misc_reature /294529976 // Attaindard_name="AI027942" // note="100% identity EST ov84a10.x1" // note="100% identity EST ov84a10.x1" // note="00811 2 excellent exon, frame 2" // repeat_region complement(3068230733) // rpt_family="MIR" // note="note" family="MIR" // note="note"	misc_feature complement(2876928838) /note="GRAIL 2 excellent exon, frame 0" repeat_region 289729214 /rpt_family="Alu" misc_feature join(2948529559,2959829779) misc_feature join(2948529559,2959829779)	repeat_region 27142805 /rpt_family="Alu" repeat_region 2804028066 /rpt_family="Alu" repeat_region 2804028066 /rpt_type=tandem /rpt_unit=A repeat_region 2871228930"	repeat_region complement(2463924694) repeat_region complement(2463925713) repeat_region complement(2572726471) repeat_region complement(2572726471) repeat_region complement(2572726471)	repeat_region 2302223326 FOSSILLE REPEAC /rpt_family="Alu" repeat_region 2347323761 /rpt_family="Alu" repeat_region 2374423767 /note="(A)24"	repeat_region 2201722038 /note="(A)22" /rpt_type=tandem repeat_region 223122457 /rpt_family="Alu" repeat_region complement(223822981) /standard name="nonesthie repeat"

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                                                                                                                                                                                                                                                                                            Submitted (24-0TL-1998) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
On Jul 24, 1998 this sequence version replaced 9i:3241936.
On Jul 24, 1998 this sequence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20950, USA e-mail address: humgenetigr.org. The orientation of the sequence is from Sp6 end to T7 end. Genes were identified by a combination of five methods including: XGRALI (available by anoxymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gommic.stanford.Edu/~chris/GENSCANW.html)searches of the complete sequence against a peptide database and the Human gene Index database at TIGR (http://www.tigr.org/tdb/hgi/hgi.html).
Genes without pepetide homolgy having spliced EST hits are termed 'Unknown gene product'. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
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Homo sapiens Chromosome 16 BAC clone CIT987SK-A-952F10, complete
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1 (bases 1 to 216021)
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3 (bases 1 to 216021)
Adams, M.D. and Loftus, B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (O2-JUN-1998) The Institute for Genomic Research,
Medical Center Dr, Rockville, MD 20850, USA, Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 216021)
Adams, M.D. and Loftus, B.J.
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AC004787.1 GI:3337381
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/note="78%-100% protein identity GenPept:U18937"
complement 38069...38215)
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44379. .44507))
                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/note="7608, STS1-cSRL-24gl-uA/cSRL-24gl-uZ, Chr. -,
                                                 /db_xref="dbSTS:G02280"
                                                                                               /note="7766, STS1-cSRL-27g3-uA/cSRL-27g3-uZ,
                                                                                                                        /clone="A-952F10"
27765. .27872
                                                                                                                                                                            /map="#16q21-22"
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Pred. No. 3.54e-02;
31; Mismatches 15;
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Best Local Similarity 13.1%;
Matches 13; Conservative
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                                                              GGGTCTGGGCTGCCCTTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGG
CCGGGTA-TGACTTTGCAACTGAAGCTG 109
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E04076
                                                                                                                                                                                                                                                                                                OS Hepatitis C virus
PN 1992349885-A/1
PD 04-DEC-1992
PF 29-WAY-1991 JP 1991152169
PI WORINAGA TSUTAE, CHAYAMA KAZUAKI, KUMADA HIROMITSU,
PI KARAWA YATAKO
PC C12N15/10,C12Q1/68,C12Q1/70//C12N15/11;
CC strandedness: Single;
CC topology: Linear;
CC topology: Linear;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepatitis C-like viruses.
1 (bases 1 to 565)
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/db_xref="dbSTS:G09935"
199463...199572
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175810. .175945
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/db_xref="taxon:11103"
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Pred. No. 3.54e-02;
52; Mismatches 33
                                                                                                                               Score 25; DB 25; L¢
Pred. No. 1.35e-01;
29; Mismatches 28;
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Map and sequence oriented from telomere to centromere. This accession is comprised of overlapping cosmids R29828 (bases 1 to 40,974) and F25496 (bases 23.336 to 60,966). R29828 is separated from cosmid F25496 (A0004475) to the left by a sequence gap of approximately 14 kb, which is to be filled by sequencing a restriction fragment from cosmid R7736 (currently in progress). Cosmid P25496 is separated from cosmid R7736 (currently in progress). Cosmid P25496 is separated from cosmid R7736 (currently in progress).
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1 (bases 1 to 60966)

Lamerdin, J.E., McCready, P.M., Skowronski, E., Viswanathan, V., Burkhart-Schultz, K., Gordon, L., Dias, J., Ramirez, M., Stilwagen, S., Phan, H., Velasco, N., Do, L., Regala, W., Terry, A., Garnes, J., Dauganan, L., Erler, A., Christensen, M., Georgescu, A., Avila, J., Liu, S., Attix, C., Andreise, T., Trankheim, M., Amico-Keller, G., Coefield, J., Duarte, S., Lucas, S., Bruce, R., Thomas, P., Quan, G., Kronmiller, B., Arellano, A., Sanders, C., Ow, D., Nolan, M., Trong, S., Kobayashi, A., Olsen, A.S. and Carrano, A.V.

Sequence analysis of a 2 Mb contig in 19p12 between UBA52 and
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Submitted (04-JAN-1999) Joint Genome Institute, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
4 (bases 1 to 60966)
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Submitted (28-OCT-1997) Human Genome Center, Joint
Institute, Lawrence Livermore National Laboratory,
Livermore, CA 94551, USA
(bases 1 to 60966)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www-bio.llnl.gov/genome/genome.html.
Location/Qualifiers
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                                                                                                                                                                                         /rpt_family="Alux" 930. .1066
                                                                                                                                                                                                                                                                                                                                                                                                                         /map="19p12 between UBA52 and D198455."
/cell_line="UV5HL9-5B for F25499, and 5H12-B for R29828"
/clone_lib-"LL19NC02 (for F25499) and LH19NC03 (for R29828) chromosome 19-specific cosmid libraries"
/note="Cosmid libraries constructed at LLNL from flow-sorted chromosomes from human-hamster hybrid cell lines UV5HL9-5B and 5HL2-B, each of which carries chromosome 19 as its only human chromosome."
                                                                                    /rpt_family~"FLAM_C"
complement(1148, .13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="R29828-F25496"
/chromosome="19"
                complement(1148. .1315)
/note="predicted exon, program: grail2exons_human_1.3,
                                                                                                                                                                                                                                                                                                                                                rpt_family="AluJo"
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7000 East Ave.,
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/product="R29881"
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/product="R29881"
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/db_xref="PDD:94106983"
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SOOTPYWHCRLIFOLAQLHTLEKDLVSACDLLGVGAEYAKVVGSEYTRALFILSKGML
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LKGTOCTQTISTIHDDEILPSNRADLFHMLFKEHHCUYYLVTYTYHSHAQAGYLEKAQ
KYTDKALMQLEKIKNLDCS9ILSSFOYILLEHILMCRLYTGHKATALQEGIYCVSVNC
MUNAEAGTYTALLRISLERINGHSTSYGVILLCHILMCRLYTGHKATALQEGIYCVSVNC
MUNAEAGTYTALRISLERINGHSTSYGVILCHIRGSNNMVVPAMQLASK IPDMSYGL
KSTLKHSNAADLNRLTAGCSLYLLGHITYYLGHRESNNMVVPAMQLASK IPDMSYGL
KSSALLRDLKKACGNAMDAHEAAQMHQNFSQOLLODHIEAGSLEHNLITSHTENDENTETT
                                                                                                                                                                                                                                                                                                                                                                                             /note="predicted exon, program: grail2exons_human_1.3, frame: 0, quality: excellent, score: 94.000--DbS similarity to overlapping ESTS:-(8155. .8237) AA963316 UI-R-E1-gi-c-06-0-UI.S1 UI-R-E1 Rattus norvegicus cDNA clone UI-R-E1- qi-c-06-0-UI 3'; (400. .482); 888 identity.--(8155. .8240) AA893275 EST197078 Normalized ratkidney, Bento Soares Rattus sp. cDNA clone RKIBE38 3' end; (420. .505); 85% identity."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="DDS similarity to overlapping ESTS:-AA963316 UI-R-E1-gi--06-0-UI-S1 UI-R-E1 Rattus norvegicus cDNA clone UI-R-E1- gi-c-06-0-UI 3'; (304. .399); 898 identity. --AA893275 EST197078 Normelized rat kidney, Bento Soares Rattus sp. cDNA clone RKIBE38 3' end; (324. .419); 898 identity. --(6480. .6660) predicted exon, program: grail2exons_human_1.3, frame: 2, quality: excellent,
/note="predicted exon, program: grail2exons_human_1.3,
frame: 2, quality: excellent, score: 83.000"
complement(8872...8996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  score: 76.000"
8155. 8249
                                                                                                                                                       /rpt_family-"Alusc"
8778. .8837
                                                                                                                                                                                                                                                                  /rpt_family="AluJb"
8480. .8768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(5602. .5883)
/rpt_family="AluJo"
6480. .6575
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Nocke-"DDS similarity to overlapping Ests:-AA963316

UI-R-E1-g1-c-06-0-UI.S1 UI-R-E1 Rattus norvegicus cDNA

clone UI-R-E1- g1-c-06-0-UI 3'; (238. 303); 888

identity.--AA89275 EST197078 Normalized rat kidney, Bento
Soares Rattus SP. CDNA clone RKIBE38 3' end; (258. 323);

888 identity."
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/note="predicted exon, predicted 
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10156. .10183,10562. .10717,11845. .11991,12086. 12176,
13147. .13250,14614. .14679,18199. .18248,18465. .18542,
18635. .18746,23665. .23755,24574. .24709,37283. .37493,
note-"Hypothetical human protein (partial)"
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2105. .2406
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RESULT 12
LOCUS
DEFINITION
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NID
VERSION
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                                                                                                                                                                                                                                                                                                                       Local Similarity 85.7%; es 30; Conservation
                                                      A62989 60
Sequence 1 from 1
A62989
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9494..96
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9052. 9196
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frame: 1, quality: excellent, score: 86.000"
10562. .10721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="predicted exon, program: grail2exons_human_1.3, frame: 0, quality: excellent, score: 100.000"
18635. .18746
/note="predicted exon, program: grail2exons_human_1.3, frame: 2, quality: excellent, score: 97.000"
complement(19286. .19309)
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18199 .18248
/note="predicted exon, program: grail2exons_human_1.3, frame: 0, quality: excellent, score: 89.000"
18465 .18542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"predicted exon, program: grail2exons_human_1.3, frame: 0, quality: excellent, score: 100.000" [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16747] [16463..16
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complement(20344. .20655)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="Aluy"
20234. .20341
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frame: 0, quality: excellent, score: 97.000"
12086. .12176
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frame: 1, quality: excellent, score: 96.000"
13147. 13550
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10156. .10183
   GI:3716861
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Pred. No. 1.35e-01;
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Mustela vison GT dinucleotide repeat, chromosome 1q.
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39 AGGGG 35
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Mustela vison GT dinucleotide repeat, chromosome lq.
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BOEHRINGER MANNHEIM GMBH (DE)
LOCATION/QUAlifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.

[ bases 1 to 1055]
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Similarity 10.8%;
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1 221 c 210 g
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gaggatcctaccgctgttgag"
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                                                                               chromosome 2.
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Seo.H.C., Willems,P.J., Kretz,K.A., Martin,B.M. and O'Brien,J.S. FUCOsidosis; four new mutations and a new polymorphism 93278392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMPFUCAS 3290 bp DNA
H.sapiens fucosidase pseudogene.
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alpha-L-fucosidase; lysosomal hydrolase; lysosome; pseudogene.
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1 (bases 1 to 1056)

Brusgaard,K., Shukri,N.M., Malchenko,S., Koroleva,I. and Lohi,O. Direct Submission
Submitted (27-JAN-1997) Breeding and Genetics, Danish Institute of Animal Science, Blichersalle K25, Tjele 8830, DK
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a 221 c 210 g 22
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735. .2761
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735. . . 2761
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                                                                                                                                                                                                                                                                                       Location/Qualifiers
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RESULT
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ID V84366 standard; cDNA to mRNA; 439 Bp.

AC V84366

DT 30-MAR-1999 (first entry)

DE Human stomach carcinoma cDNA clone HP10408.

Transmembrane protein; HP10408; human; stomach cancer; ds.

NS Homo sapiens.

H Key
T CDS
T PN W09855508-A2.

PD 10-DEC-1998.

PP 03-JUN-1998; J02445.

PF 03-JUN-1998; J02445.

PR 03-JUN-1997; JP-144948.

PR 03-JUN-1997; JP-144948.

PR 03-JUN-1997; JP-144948.

PR (SAGA) SAGAMI CHEM RES CENTRE.

PR (KACOS) SAGAMI CHEM RES CENTRE.

PI KATOS S, Sekine S, Yamaguchi T;

PR WPI: 99-045730/04.

PR P-PSDB; W88498.

PT New human proteins containing transmembrane domains and their rencoding sequences - useful in the preparation of antibodies and PT large-scale protein production, gene diagnosis, and gene therapy Claim 4; Page 135; 178pp; English.

CC This is the nucleotide sequence of CDNA clone HP10408, which cincludes a coding region (also claimed) for a novel human cransmembrane protein (see W88498). The clone was isolated from a commentative signal sequence and a putative method, and by protein synthesis by in vitro translation. The cencoded protein has a putative signal sequence and a putative content transmembrane domain. The invention provides nucleotide contents (see V84359-76) coding for 18 transmembrane proteins Location/Qualifiers 75..311 /*tag- a /*tog- "cDNA comprising the coding region (minus the stop codon) is claimed (Claim 3)"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
EP-571911-A.
01-DEC-1993.
24-MAY-1993; 1
26-MAY-1992; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (see W88491-508), vectors containing such polynucleotides, and eukaryotic cells containing the vectors. The proteins can be used as antigens or as compositions in the preparation of antibodies against the proteins. The polynucleotides can be used as probes for gene diagnosis, and as gene sources for gene therapy and large-scale production of proteins encoded by the cDNA. The host cells are used for the detection of ligands corresponding to the expressed proteins, and the screening of low mol.vr. medicines. Sequence 439 BP; 89 A; 137 C; 109 G; 104 T;
                                                                                                                                                                                                                                                                                                          Claim 3; Page 14; 23pp; English.

Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (051735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also 051735-45 and 051747-59.

Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                      N81164 standard; DNA; 204 BP.

N81164;

08-NOV-1990 (first entry)

Base substituted E.coli beta-galactosidase alpha-fragment.

E.coli beta galactosidase alpha-fragment; base substitutions;

Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                            New oligo:nucleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shank DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q51746 standard; cDNA; Q51746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAY-1994 (first
                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 tggcagctcacatggaacagggccgggtatgactttgcaactgaagctgaaggtgtattt 175
                                                                                                                                                                                           133 GGAACTTGTCAGAAAAGACTCCTTCAGCTTCAGTTGCAAAGTCATACCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56
                                                                                                                                                                                                                       11 ssvhsyyvvhvvshhhsvhhvvhhvhvsv-vvvhhvvhvvhhvhyhvyvsvc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCCTCTTGACCCCTCCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T ) BECTON DICKINSON CO.
k DD, Spears PA;
93-378844/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            totgacaaattootootatgagtooagottootggaattgottgaaaagototgootoot 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTGACAAGTTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 98.9%;
1 Similarity 99.4%;
179; Conservative
                                                                                                                                                                                                                                                    Similarity
1; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-889651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108325
                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probe MK14-A
; DNA probe; mycobacteria; disease diagnosis;
                            Location/Qualifiers 19..69
/function=multiple cloning site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           be MK14-A
                                                                                                                                                                                                                                                                  20.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91
                æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 178; DB 60;
Pred. No. 4.41e-99;
                                                                                                                                                                                                                                                                  Score 37; DB 9;
Pred. No. 1.15e-
                                                                                                                                                                                                                                                     46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                     5e-08
                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                 Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 439;
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C Random point mutations were introduced into the alpha fragment of C Random point mutations were introduced into the alpha fragment of C E. coli beta-galactosidase. The wild type sequence was obtained as a constant of the collect of th
                                                                                 Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                     EP-571911-A.
01-DEC-1993;
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
Shank DD, Spears PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP-285123-A.
05-MAY-1988.
30-MAR-1988; 105163.
03-APR-1987; US-034819.
                                                                                                                                                  (051735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.

Sequence 91 Bp; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Introducing random point mutations into nucleic acods by prepn of single stranded template, annealing a primer, misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer_bind
                                                                                                                                                                                                                                                                Claim 3: Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides (Q51735). It hybridized to all spp. of mycobacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q51746 standard; cDNA; Q51746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J,
                                                                                                                                                                                                                                                                                                                                                      WPI; 93-378844/48.
New oligo:nucleotide probes detection and amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide; DNA probe; mycobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide probe MK14-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                   samples
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 CCTGTTCCATGTGAGCTGCCAAGGAGGGTCAAGAGGAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 ymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynv 145
                                      12 svhsyyvvhvvshhhsvhhvvhhvhvhvvhhvvhhvhyhvyvsvctcaagc
  52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hnhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvhc 186
  GACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGC
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                                                                                                              Similarity
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                                                                                   18.9%;
|larity 10.7%;
|Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 1; I
Pred. No. 1.15e-08;
54; Mismatches 39
                                                                                        Score
Pred.
39; M
                                                                                                                                                                                                                                                                                                                                                      specific for Mycobacteria of Mycobacteria nucleic ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 C;
                                                                                      re 34; DB 9; Le
1. No. 5.55e-07;
Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bamford J, Reinikainen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39;
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                                                                                                                                   Length 91;
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acid
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d in
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                                                    67
                                                                                             Gaps
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Best Local s
Matches
W09418318-A.
18-AUG-1994.
01-FEB-1994;
01-FEB-1993;
30-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                               LT 6
Q70467 standard; DNA; 114
Q70467;
                                                                                                                                                                                                                                                                                             Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding defector domain; concateneated heterofunctional protein; linked direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Random point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host vector system. The sequence covers all 176 difft base substitutions, most of which
                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                           05-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  occurred singularly in any given mutant. See also P80575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Introducing random point mutations into nucleic acods - by prepn of single stranded template, annealing a primer, misincorporation, completion of molecules and screening.
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05-WAR-1988.
05-WAR-1988; 105163.
03-APR-1987: US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E.coli beta galactosidase alpha-fragment; base substitutions; Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; p; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 88-279927/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 ccbnnhvchnvhbnnhrnwayvrhdarrddvhc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 yrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvhnhnncnc 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCCTCTTGACCCTCCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGCAGCTCACATGGAACAGGGCCGGGTATGAC
; US-013416.
; US-176500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP;
                                                                                                                               /*tag= a
/note= *this sequence represents 'Z'; Z
ceruence of 6, 9 or 12 nucleotides (see
                                                                                                                            sequence of 6, comments)"
                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function=multiple cloning 187..204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
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Pred. No. 1.99e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204;
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                                                                                                                                                                        can
                                                                                                                                                                                                                                                                                                                           linker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    elongation
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                                                                                                                                                                                                                                                                                                                                                    domain;
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J4; U00977.

J0-DEC-1993; US-013416.

J0-DEC-1993; US-176500.

R 31-JAN-1994; US-189331.

PA (UYNC-) UNIV NORTH CAROLINA.

PI FOWLKES DM, KAY BK;

NR WPI; 94-279739/34.

P-PSDB; R58378.

Identifying promise.
                 TRESULT

TRESULT

TRESULT

ACCORD

ACC
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Best Local
Identifying proteins or peptide(s) which bind a ligand screening a recombinant vector library expressing fusio comprising a binding domain and an effector domain bisclosure; Page 36; 255pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding doi effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
Key
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Q70470;
10-APR-1995 (fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
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(UYNC-) UNIV NORTH CAR
FOWLKES DM, KAY BK;
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5; Conser
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/note= "encoded
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P;     0 A;     2 C;     2 G;     2 T;
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Pred. No.
30; Misma
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proteins
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US-09-092-296-3.rng

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CC 970470 is a generic DNA sequence used to generate random TSAR (Totally CS Synthetic Affinity Reagents) peptides. This generic formula can also be CC represented as follows: X(NNB) 4(CAC) (NNB)4(CAC) (NNB)56(CAC)(NNB)6 CC (NNB)58 CC (CAC)2(NNB)8. X and Y are flanking restriction sites (X is not the same CC as Y) that are not specified further. The peptides generated by this and CC cher generic sequences (07047-73) have invariant histidine residues CC incorporated into variant sequences. TSARs are concatenated CC regions - a binding domain with affinity for a ligand and a second CC effector peptide portion that is chemically or biologically active. They CC may further comprise a linker peptide between the 2 domains. The TSARs CC or compsns. comprising a TSAR binding domain can be used in vivo to CC deliver a chemically or biologically active molety, eg. metal ion, CC radioisotope, peptide, toxin or enzyme, to the specific target or on the CC cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need CC comps are easily characterised and have designed activity allowing direct and rapid detection in a screening process. SQ Sequence 114 BP; 5 A; 10 C; 0 G; 0 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <del></del>
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PT Identifying proteins or peptide(s) which bind a ligand - by PT screening a recombinant vector library expressing fusion proteins PT comprising a binding domain and an effector domain PS Disclosure; Page 36; 255pp; English.

CO 70470 is a generic DNA sequence used to generate random TSAR (Totally CC Synthetic Affinity Respents) peptides This generic formula can also be CC represented as follows: X(NNB)4(CAC)(NNB)4(CAC)(NNB)8Z(NNB)8(CAC)(NNB)8.

C. (CAC)2(NNB)Y. X and Y are flanking restriction sites (X is not the same CC as Y) that are not specified further. The peptides generated by this and CC other generic sequences (Q70471-73) have invariant histidine residues CC incorporated into variant sequences. TSARs are concatenated by this and CC other generic sequences (Q70471-73) have invariant histidine residues CC incorporated into variant sequences. TSARs are concatenated by this and CC effector peptide boration that is chemically or a ligand and a second cregions - a binding domain with affinity for a ligand and a second cregions - a binding domain with affinity for a ligand and a second cregions - a binding domain with affinity for a ligand and a second cregions - a binding domain with affinity for a ligand and a second cregions - a binding domain she the Z domains. The TSARs CC or compsns. comprising a TSAR binding domain can be used in vivo to
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Best Local
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01-FEB-1994; U00977.
01-FEB-1994; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROL
FOWLKSS DM, KAY BK;
WPI; 94-779739/34.
P-PSDB; R58378.
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Q70470;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          direct;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bnnbnnbnnbnnbcacnnbnnbnnbnnbnnbnnbnnbc 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rapid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection;
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/note=
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6.7%;
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Pred. No.
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W09418318-A.
18-AUG-1994; U00977.
01-FEB-1994; U5-013416.
01-FEB-1993; US-013416.
30-DEC-1993; US-175500.
31-JAN-1994; U5-189331.
(UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, Kay BK;
WPI; 94-779739/34.

P-PSDB; R65153

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 5 A; 10 C; 0 G; 0 T;
                                                                                                                     Q70467;
Q70467;
Q5.APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding d
effector domain; concateneated heterofunctional protein; linke
effector domain; concateneated heterofunctional protein; linke
                                                                                                                                                                                                                                    Q70467
                                                                                                         Synthetic.
                                                                       misc_feature
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                                                                                                                                                                                                                                                                                                         TGGCAGCTCACATGGAACAGGGCCGGGTATGAC
                                                                                                                                                                                                                                                                                                                                                                                                              CAGGAGCGCAGTGGCCACTATGGGGTCTGGGCCTGCCCTTGTCCTCCTTGACCCTCCT
                                                                                                                                                                                                                                    standard; DNA; 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
/*tag= a
/note= "this sequence represents 'Z'; Z
sequence of 6, 9 or 12 nucleotides (see
comments)"
                                                                       Location/Qualifiers 55..60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.1%;
                                                                                                                                                                                                                                      ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 29; I
Pred. No. 2
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2.96e-04;
                                                                                                                                                                                                                                                                                                               93
                                                                                                                                                                                                                                                                                                                                                                                                                                                              61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 114
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                                       can
                                                                                                                                              linker;
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                                       be
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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PT Identifying proteins or peptide(s) which bind a ligand - by PT Identifying proteins or peptide(s) which bind a ligand - by Identifying proteins proteins processing a binding domain and an effector domain PS Disclosure; Page 35; 255pp; English.

PS Disclosure; Page 35; 255pp; English.

CC 270467 is a generic DNA seguence used to generate random TSAR (Totally CC Synthetic Affinity Reagents) peptides. This generic formula can also be CC and y are flanking restriction sites (X is not the same as Y) that are CC and y are flanking restriction sites (X is not the same as Y) that are CC cont specific peptides generated by these generic sequences are shown in C70466-68.

CC Other specific peptides generated by these generic sequences are shown in C70466-68.

CC comprising at least two functional regions - a binding domain with CC caffinity for a ligand and a second effector peptide portion that is comprising at least two functional regions - a binding domain with CC comprising at least two functional regions - a binding domain with the expressed peptide contains 2 or 4 cystelne residues positioned CC in, or flanking, the unpredicted or variant residues of the TSAR sides or compans. comprising a TSAR binding domain can be used in vivo to compans. comprising a TSAR binding domain can be used in vivo to call other a chemically or biologically active moiety, eg. metal ion, can be captured to the peptides. The TSARs or complex methods of hybridoma formation or flarget or on the cell. They can also replace the function of macromolecules, eg. compocional or polyclonal antibodies and therefore circumvent the need for the TSARs are easily characterised and have designed activity allowing CC direct and rapid detection in a screening process.

QS

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δÃ В

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I Identifying proteins or peptide(s) which bind a ligand - by
FT Screening a recombinant vector library expressing fusion proteins
Comprising a binding domain and an effector domain
PS Disclosure; Page 35; 25pp; English.
CQ 70469 is a generic DNA sequence used to generate random TSAR peptide
CC This generic formula can be represented as follows: X(TGC)(NNB)10-
CC (TGC)(NNB)2(TGC)(NNB)14(TGC)Y. X and Y are flanking restriction
CC sites (x is not the same as y) that are not specified further. This
CC sequence generates peptides that are cloverleaf in structure. Other
CC generic sequences are shown in Q70465-68. Other specific peptides
CC generated by these generic sequences are shown in R65150-54. TSARS are
CC generated by these generic sequences are shown in R65150-54. TSARS are
CC concatenated heterofunctional proteins or peptides, comprising at least
CC a second effector peptide portion that is chemically or biologically
CC active. They may further comprise a linker peptide between the 2 domains.
CC active. They may further comprise a linker peptide between the 2 domains.
CC contains 2 or 4 cysteine residues positioned in, or flanking, the
CC conformational rigidity to the peptides. The TSARS or compsis. comprising
CC a TSAR binding domain can be used in vivo to deliver a chemically or
CC all therefore contents are ensured in on, radioisotope, peptide, toxin
CC the function of macromolecules, eg. monoclonal or polyclonal antibodies
CC and therefore circumvent the need for complay methods of the incidence.
                                Matches
                                            Query Match
Best Local Similarity
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18-AUC-1994; U00977.
01-FEB-1994; U00977.
01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLIFOWLKS DM, KAY BK;
WPI: 94-279739/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JLT 10
Q70469 standard; I
Q70469;
Q7-APR-1995 (fir:
                                                                                                                                              the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                  detection in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 GGGGTCTGGGCCCCTTTCTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGG 81
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                            Conservative
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/note= "this sequence r
sequence of 6,9 or 12 n
comments)"
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                                              15.6%;
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                                                                                                             4 C;
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                                                 28; DB 12; Length 114; No. 1.00e-03;
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2.96e-04;
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                                                                                                             4 T;
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Q70465;
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63
                                     69 bnnbnnbnnbnnbnnbnnbnnbnnbnnbnnb 102
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                                                                             GGAGCGCAGTGGCCACTATGGGGTCTGGGCCTGCCCTTGTCCTCCTTGACCCTCCTTG
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В

9 banbanbanbanbanbanbanbtgcanbanbanbanbanbanbanananananbanbtg 68

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PT Identifying proteins or peptide(s) which bind a ligand - by
PT screening a recombinant vector library expressing fusion proteins
PT comprising a binding domain and an effector domain
PS Disclosure; Page 35; 255pp; English.
CC 070465 is a generic DNA sequence used to generate random TSAR (Totally
CC Synthetic Affinity Reagents) peptides. This generic formula can also be
CC crepresented as follows: X(NNB)6(TGC)(NNB)112(NNB)14(TGC)(NNB)3Y. X
CC and Y are flanking restriction sites (X is not the same as Y) that are
CC contespecified further. Other generic sequences are shown in 070466-68.
CC Other specific peptides generated by these generic sequences are shown in
CC R65151-54. TSARS are concatenated heterofunctional proteins or peptides,
CC comprising at least two functional regions - a binding domain with
CC affinity for a ligand and a second effector peptide portion that is
CC comprising at least two functional regions - a binding domain with
CC affinity for a ligand and a second effector peptide portion that is
CC comprising a result of a second effector peptide portion that is
CC confers on the 2 domains. The oligonucleotides are also designed so
CC that the expressed peptide contains 2 or 4 cysteine residues positioned
CC confers some degree of conformational rigidity to the peptides. The TSARS
CC confers some degree of conformational rigidity to the peptides. The TSARS
CC conformation of macromolecules, eg.
CC radioisotope, peptide, toxin or enzyme, to the specific target or on the
CC celiver a chemically or biologically active molety, eg. metal ion,
CC conjons or polyglonal antibodies and therefore circumvent the need
CC conjons methods of hybridoma formation or in vivo antibody
CC production. The TSARs are easily characterised and have designed
CC activity allowing direct and rapid detection in a screening process.
                                                                                                                                                                                                                activity allowing Sequence 114 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding ceffector domain; concateneated heterofunctional protein; linke
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                                                                       Local Similarity 2.1%; es 2; Conservative
GCAGCTCACATGGAACAGGGCCGGGTATGACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       canbanbanbanbanbanbanbanbanbanb 102
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US-176500.
US-189331.
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                                                                                                                                                                                                                direct and rapid detection in a screening; 0 A; 2 C; 2 G; 2 T;
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                                                                                                         15.6%;
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                                                                                                         Score 28; DB 12;
Pred. No. 1.00e-0
                                                                           28;
                                                                       Mismatches
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treatment; generic; ss.
                                                                                                         00e-03;
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                                                                       64;
                                                                       Indels
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PT Identifying proteins or peptide(s) which bind a ligand - by proteins are combinant vector library expressing fusion proteins processing a binding domain and an effector domain proteins processing a binding domain and an effector domain proteins processing a binding domain and an effector domain proteins processing a binding domain and an effector domain random TSAR (Totally CC 2070468 is a generic DNA sequence used to generate random TSAR (Totally CC 2070468 is a generic DNA sequence used to generate formula can also be considered as foliows: X(NNB)1(TGC)(NNB)5Z(NNB)7(TGC)(NNB)5LOY: X CC 2070468 is a generic bnA sequence save shown in 070466-68.

CC cont specific peptides generated by these generic sequences are shown in 070466-68.

CC control specific peptides generated by these generic sequences are shown in 070466-68.

CC control specific peptides generated by these generic sequences are shown in 070466-68.

CC comprising at least two functional regions - a binding domain with CC comprising at least two functional regions - a binding domain with the comprising at sective. They may further comprise a linker CC comprising a todomain schedy may further comprise a linker CC conference of the unpredicted or variant residues positioned CC in, or flanking, the unpredicted or variant residues. These residues CC confers some degree of conformational rigidity to the peptides. The TSARS CC complex methods of hybridoma formation of macromolecules, eg. metal ion, cc radiciscope, peptide, toxin or enzyme, to the specific target or on the CC call. They can also replace the function of macromolecules, eg. metal complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity CC control of the peptides. The control of Activity of the control of Activity o
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Best Local s
Matches
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30-DEC-1993; US-175500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWLKS-DM. KAY BK;
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TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
synthetic.
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Q70468;
Q5-APR-1995 (first en
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                                         T76405 standard; DNA; 178
T76405;
15-SEP-1997 (first entry)
      Asthma;
                         Human endothelin-1
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                                                                                                                                                                                                                                                             107
                                                                                                                                                                                                                    63
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                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                               GCTTCAGTTGCAAAGTCATACCCGGCCCTGTTCCATGTGAGCTGCCAAGGAGGGTCAAGA 48
ndothelin-l antisense oligonucleotide. airway epithelium; adenosine free: rv
                                                                                                                                                                                                                                                                                                                                                                                                                                   114 BP;
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                                                                                                                                                                                                                                                                                                                                                Conservative
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/note= "this
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                                                                                       ВP
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Pred. No. 1.
30; Mismatc
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6, 9 or 12 nucleotides (see
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                                                                                                                                                                                                                                                                                                                                                                                                                                   a screening process. 2 G; 2 T;
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    cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                          Length 114;
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                                                                                                                                                                                                                                                                                                                                                Gaps
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Best Local
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07-JUN-1995; US-474497.
(UYEC-) UNIV EAST CAROLINA.
Metzger WJ, NYCE JW;
WPI; 97-051871/05.
                                                                                                                                                                      W09418318-A.
18-AUG-1994; U00977.
01-FEB-1994; US-013416.
01-FEB-1993; US-176500.
30-DEC-1993; US-176500.
31-JAN-1994; UNIV WORTH CAROLINA.
Fowlkes DM, Kay BK;
WPI; 94-79739/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A method for treating airway disease in a subject has been produced, which involves the topical administration of an essentially adenosine free antisense oligonicleotide (ON) to the airway epithelium of the subject. The present sequence is an antisense oligonicleotide specific for the human endothelin-1, targeted at the initiation codon. The method can be used to treat airway diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary disease, bronchitis and other airway diseases characterised by an inflammatory response. By eliminating adenosine from the antisense ON, its liberation upon antisense degradation is prevented, thereby preventing adenosine-induced bronchoconstriction in patients with hyper-reactive airways. Sequence 178 BP; O A; 52 C; 46 G; 32 T;
                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5;
A method
p-pSDB; R65154.

Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain Disclosure; page 35; 255pp; English.

Q70468 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides This generic formula can also be represented as follows: X(NNB)11(TGC)(NNB)52(NNB)10°. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chronic obstructive pulmonary disease; bronchitis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Generic DNA sequence to génerate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding dom refector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q70468; tandard; DNA; 114 BP. Q70468;
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Similarity 25.0%;
18; Conservative
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/note= "this sequence represents '2'; 2 can
sequence of 6, 9 or 12 nucleotides (see
comments)"
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1.00e-03;
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REFERENCE OCCURS TERMINATER TO COCCURS TO THE PROPERTY OF THE 
pr Identifying proteins or peptide(s) which bind a ligand - by
Pr screening a recombinant vector library expressing fusion proteins
Pr comprising a binding domain and an effector domain
PS Disclosure; Page 35; 255pp; English.
CC 07/0465 is a generic DNA sequence used to generate random TSAR (Totally
CC Synthetic Affinity Reagents) peptides This generic formula can also be
CC represented as follows: X(NNB)6(TGC)(NNB)11Z(NNB)14(TGC)(NNB)37. X
CC and Y are flanking restriction sites (X is not the same as Y) that are
CC ont specified further. Other generic sequences are shown in 070466-68.
CC R65151-54. TSARS are concatenated by these generic sequences are shown in
CC comprising at least two functional regions - a binding domain with
CC chemically or biologically active.They may further comprise a linker
CC peptide between the 2 domains. The oligonucleotides are also designed so
CT that the expressed peptide contains 2 or 4 cysteine residues positioned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC Other specific peptides generated by these generic sequences are shown in CR 865151-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with CC affinity for a ligand and a second effector peptide portion that is CC chemically or biologically active. They may further comprise a linker CC peptide between the 2 domains. The oligonuclectides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned CC confer some degree of conformational rigidity to the peptides. The TSARs CC or comprise, comprising a TSAR binding domain can be used in vivo CC radiolsotope, peptide, toxin or enzyme, to the specific target or on the CC cell. They can also replace the function of macromolecules, eq. monoclonal or polyclonal antibodies and therefore circumvent the need CC for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity CC allowing direct and rapid detection in a screening process.
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01-FEB-1994; U00977.
01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UVNC-) UNIV NORTH CAROLINA.
FOWLKES DM, KAY BK;
WPI; 94-279739/34.
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070465;
Q70465;
05-APR-1995 (first entry)
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/note= *this sequence represents 'Z'; Z
sequence of 6, 9 or 12 nucleotides (see
comments)*
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Pred. No. 3.36e-03;
26; Mismatches 61
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                                                                                                                                                                                                   in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or composis, comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need
                                                                                                  for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
                               Similarity
                            15.0%;
                                                     Length 114;
0;
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Conservative
Score 27; DB 12;
Pred. No. 3.36e-03
29; Mismatches 7
 76;
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- 63 bnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbtgcnnbnnb 111
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itle: escription:	>US-09-092-296-3 (1-180) from US09092296.seq
A. Sequence:	1 CAGGAGCGCAGTGGCCACTACTTGAAAAGCTCTGCCTCCT 180

Rui Tal Tii Dei Pei Comp: GTCCTCGCGTCACCGGTGAT......GAACTTTTCGAGACGGAGGA

Scoring table: TABLE default Gap 6

Nmatch STD: Dbase 0; Query 0

165359 seqs, 43243793 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-issued 1:5A_COMB 2:5B_COMB 3:5C_COMB 4:PCT9_COMB 5:backfiles1

Statistics: • Mean 7.135; Variance 3.967; scale 1.799

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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97, Appli 41, Appli	Sequence 92, Applicat Sequence 98, Applicat	~ ~	Sequence 94, Applications Sequence 100, Applicat	Sequence 142, Applicat	144,	145	1	97	99,	22	5	5, A	Sequence 14, Applicat	Sequence 22, Applicati	Description
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8-40	1650	9-03	8-84	8-84	9-03	8-84	9-03	8-84	9-03	9-03	8-84	8-84	9-03	8-84	9-03	-09-031-	8-8	-09-031	-08-847	-08-847	9-031-	9 - 031	8-847	8-847
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TYPE: nucleic acid	CHONACTENT	Tem Too.	~	TELEFAX: 212-838-3884		TELECOMMUNICATION INFORMATION:	Æ	REGISTRATION NUMBER: 30,946	NAME: Hanson, No. 5795961man D.	ATTORNEY/AGENT INFORMATION:	CLASSIFICATION:	4-FEB-1995	Z	LICATION DATA:	, Version #1.30	co		TYPE: Fl		0	COUNTRY: U.S.A.	•	New York	05 Third Ave	ADDRESSEE: Felfe and Lynch	DENCE ADDRESS	SEQUENCES:	Antibodies			Welt, Sydn	: Old, Lloyd J.	: Carr, Fr	Harris, Will	ñ	GENERAL INFORMATION:	. 5795961	Application				US-08-388-672A-22 STANDARD; DNA; UNC; 965 BP.	LT 1

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TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
SEQUENCE 965 BP; 192 A; 170 C; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
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US-08-232-463-14 STANDARD; DNA; UNC; 7218
                                             IMMEDIATE SOURCE:
CLONE: pTZgpt-F1s
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER
                                                                                                                                                                                                   APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE_DOCKET NUMBER: 30472/114 IM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           857 VRGRSYDSDGGDYWGGTTVTVSSHUVKDMTSSSSASVGDRVTTCRSSTTHGNGNTYYWYK 916
                                                                                                                  TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 GCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 16.1%;
Local Similarity 19.6%;
les 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCCTTGACC-CTCCTTG 62
           Local Similarity
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURERNT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F.G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                              TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKAKYRVSNRSGVSRSGSGSGTDYTTSSDATYYCGTHARTGGTKVKG
                                                                                  TOPOLOGY:
                                                                                            STRANDEDNESS:
                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                       RY: USA
22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                VA
 Conservative
                                                                                                                                                                     (703)683-4109
                                                                                   linear
           15.6%;
                                                                                            single
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Pred. No. 6.29e-06
Score 28; DB 2; Length 7218;
Pred. No. 2.53e-05;
90; Mismatches 66; Indels
                                                                                                                                               14 :
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                                                                                                                                                                                                        30472/114 IMMU
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                            Matches
                                      Query Match
Best Local
                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 2307
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Sequence 5, Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..215
LOCATION: 1..215
OTHER INFORMATION: /standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 AGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCCT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
18 CNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSANYNYGGNNVGAAK 77
                           Local Similarity
les 22; Conser
                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03/MAY-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEA
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGGGTCTGGGCTGCCCCTTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Steuric
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAGTTCCTCCTATG 140
                                                                                                                                                                  STRANDEDNESS: single TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
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Application US/08238163
                           15.0%;
llarity 20.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LABAVITCH, John M.
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                                                                                                                                                      protein
                            42;
                                       Score 27; DB 1; L
Pred. No. 1 01e-04;
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                              45;
                                                   Length 215;
                              Indels
                              1:
                              Gaps
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CCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTG-AAGGAGT 116

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Query Match
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OTHER INFORMATION: /standard_name= "Deduced amino acid OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMEER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-238-163-5 STANDARD; DNA; UNC; 215
                                                                                                                                       158 ATTCCAGGAAGCTGGACTCATAGGAGGAACTTGTCAGAAAAGACTCCTTCAGCTTC-AGT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 YGSSKTAMTSRNRTGKTANNAVDSRNMGDASVGSDKNTK 158
                                                                                                                                                                                                  Local Similarity 13.8%; es 22; Conservation
                                                                                                     61 YSSANYNYGGNNVGAAKTHYYTHTNVSGADSKTVTDSYNASGTSSSNGGTD-GNRSGADS 119
              39 AGGGGCAGCCCAGACCCCATAGTGGCCACTGCGCTCCTG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READALE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                      1 MTNVTMSSSSVVSRTASCNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNK 60
                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LABAVITCH, John M. APPLICANT: POWELL, Ann APPLICANT: STOTZ, Henrik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BENNETT, Alan
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: Single
                                                                         TGCAAAGTCATACCCGGCCCTGTTCCATGTGAGCTGCCAAGGAGGAGGACAAGAGGAGACA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Steuart Stre
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                      Score 27; DB 1; Length 215;
Pred. No. 1.01e-04;
66; Mismatches 69; Indels
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Sequence 99, Application PC/TUS9511934
Sequence 99, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. GENERAL IN
                                                                                                                 PCT-US95-11934-99 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
SEQUENCE 965 BP; 192 A; 170 C; 226 G; 200 T; 177 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22, Application US/08388672A Sequence 22, Application US/08388672A Patent No. 5795961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-388-672A-22 STANDARD; DNA; UNC;
                                                                                                         XXXXX
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                                                                                                                                                                                                                    841 NSRSSVTAADTAVYYCVRGRSYDSDGGDYW 870
                                                                                                                                                                                                                                                                               781 GURHUVHVSGGVRSTSTCTASDYTTSYWGWVRGRGWGDYGGGYTNYNGKRGRVTMADTSS 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 212-688-920
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                93 GTCATACCCGGCCCTGT-TCCATGTGAGCTGCCAAGGAGGGTCAAGAGAGAGACAAGGGG 35
                                                                                                                                                                                    34 CAGCCCAGACCCCATAGTGGCCACTGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION NAME: Hanson, No. 57959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 14-FEB-19:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Recombination of INVENTION: Antibodies 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Old, Lloyd J. APPLICANT: Welt, Sydney APPLICANT: Kitamura, Ku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 212-688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wallace, T. Paul
APPLICANT: Harris, William J.
APPLICANT: Carr, Frank J.
APPLICANT: Old, Lloyd J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 805 Thi
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: unkno
                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hanson, No. 5795961man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
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FILING DATE:

20-SEP-1995

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Matches
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Best Local :
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TELEX: 66141 PENNIE
INPORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENCTH: 75 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
SEQUENCE 75 BP; 1 A; 1 C; 7 G; 5 T; 61 OTHER.
                                                                                                                                                                                    Sequence 97, Application PC/TUS9511934 Sequence 97, Application PC/TUS9511934 GENERAL INFORMATION:
                                                                                                                                                                                                                              XXXXXX
                                                                                                                                                                                                                                       PCT-US95-11934-97 STANDARD; DNA; UNC; 82
                                                                                                                                                                                                                                                                                                                       23 GGGTCTGGGCTGCCCCTTGTCCTCCTTGACCCTCCTTGGCAGCTCACATGGAACAGGG 82
                                                                                                                                                                                                                                                                               83 CCGGGTATG 91
                                                                                                                                                                                                                                                                                                  65 NBGGTTGTG 73
                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 20-SEP-19
CLASSIFICATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY Glisk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION NATA:
APPLICATION NUMBER: PCT/US95/11934
                                                                                                                               APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Peptide Libraries NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                          ADDRESSEE:
STREET: 11
CITY: New
STATE: New
                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                       10036
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                                                                                                              E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (212) 790-9090
(212) 869-9741/8864
                                                                                USA
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20-SEP-1995
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8.7%;
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Best Local :
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SEQUENCE 82 BP; 1 A; 2 C; 10 G; 8 T; 61 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent NO. 5773688
GENERAL INFORMATION:
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                              CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP HEI 6-71048
ETLING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 577368man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2589-024-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Local Similarity 8.7%;
les 6; Conservative
                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/418,444A
FILING DATE: 07-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKEI NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANI: ITO, KAZUTOSHI
TITLE OF INVENTION: GENE EXPRESSION VECTOR USING THE GENE
TITLE OF INVENTION: EXPRESSION REGULATING REGION OF THE ADP RIBOSYLATION
TITLE OF INVENTION: FACTOR
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANI: KURODA,
APPLICANI: HIROTA,
APPLICANI: ITO, KA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCGGGTATG 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Misrock, S. L
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08418444A
Application US/08418444A
                                                                                                                                                                                                                                                                                                                                                                                                                                     E: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (212) 869-9741/8864
(703) 413-2220
                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                703) 413-3000
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Pred. No. 7.70e-02;
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                                                         2589-024-0
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Patent No.

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Query Match 12.2%;
Best Local Similarity 72.0%;
Matches 36; Conservative
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3088 base
TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 3088 BP; 716 A; 761 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 145, Application US/08471052A Sequence 145, Application US/08471052A
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                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036-2711
COMPUTER READABLE FORM:
CMEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,052A
FILING DATE: 06-JUNE-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                            TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 145
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                                                                                                                                                                                                                                                                                     NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                      MOLECULE TYPE: DNA
QUENCE 65 BP; 3 A; 3 C; 3
                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 65 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kay, B. K.
APPLICANT: Fowkles, D. M.
APPLICANT: Fowkles, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 166
                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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TYPE: nucleic acid
STRANDEDNESS: double
                             CTGGACTCATAGGAGGAACTTGTCAGAAAAGACTCCTTCAGCTTCAGTTGCAAAGTCATA 88
                                                                                                                                                                          TOPOLOGY: un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
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1155 Avenue of the Americas
                                                                                                                                                                       unknown
                                                                                                  11.7%;
13.8%;
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Pred. No. 7
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0; Mismatches 14; Indels
                                                                                                                                            G,
                                                                                                 Score 21; DB 1; I
Pred. No. 2.73e-01;
                                                                                      16;
                                                                                                                                           2 T; 54 OTHER.
                                                                                                                                                                                                                                                                                                                     1101-179
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                                                                                      Mismatches
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                                                                                      40; Indels
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                                                                                                               Length 65;
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                                                                                             Sequence 143, Application US/08471052A
Sequence 143, Application US/08471052A
Patent No. 565503
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 66 BP; 2 A; 3 C; 4 G; 2 T; 55 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 144,
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                                                                                                                                                                                   US-08-471-052A-143 STANDARD; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 66 bases
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Local Similarity 5.2%;
ses 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, WURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,052A
FILING DATE: 06-UNE-1995
CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
CQRRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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                                          APPLICANT: Kay, B. K.
APPLICANT: Fowles, D. M.
TITLE QF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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TELEX: 66141 PENNIE
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1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                              DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S. Leslie
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Pred. No. 2.73e-01;
18; Mismatches 37;
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D.
APPLICANT: Fowlkes, D.
TITLE OF INVENTION: TO
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-471-052A-142 STANDARD; DNA; UNC; 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 142, Application US/08471052A Sequence 142, Application US/08471052A Patent No. 5625033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA SEQUENCE 68 BP; 3 A; 3 C; 5 G; 3 T; 54 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 CTGGACTCATAGGAGGAACTTGTCAGAAAAGACTCCTTCAGCTTCAGTTGCAAAGTCATA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 CCCGG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 CCTGG 68
                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 11.7%; Score 21; DB 1; I
Local Similarity 13.8%; Pred. No. 2.73e-01;
es 9; Conservative 16; Mismatches 40
                     CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEPAX: 212 869-8864/9741
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                        STREET: 1155 A
                                                                         APPLICATION NUMBER: FILING DATE: 06-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 68 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 06-JUI CLASSIFICATION: 530
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REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Misrock,
                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                   E: New York TRY: U.S.A. 10036-2711
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Misrock, S. Leslie
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1155 Avenue of the Americas
                                                                      06-JUNE-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 D. M. Totally Synthetic Affinity Reagents
                                                                                              US/08/471,052A
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                                                                                                                                        Version
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Best Local :
                                                                                              MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP; 3 A; 4 C; 3 G; 1 T; 63 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 94, Application PC/TUS9511934
Sequence 94, Application PC/TUS9511934
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA SEQUENCE 69 BP; 2 A; 4 C; 6 G; 2 T; 55 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XXXXXX
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PCT-US95-11934-94 STANDARD; DNA; UNC; 74
                                                                                                                                                                                                                                       TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 AGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCCTTGACCCCTCCTTGGCAGC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Natch 11.7%;
Local Similarity 5.2%;
Local Sim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION UNMER: PCT/US95/119
FILLING DATE: 20-SEP-195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding POTITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 11-CORK CITY: New York
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                              STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 18,872 REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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TELEX: 66141 PENNIE
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     11.7%;
llarity 1.7%;
Conservative
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Score 21; DB 4; 1
Pred. No. 2.73e-01;
20; Mismatches 39
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Pred. No. 2.73e-01
18; Mismatches 3
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       39;
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                                                  Length 74;
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Best Local
Sequence 99, Application PC/TUS9511934
Sequence 99, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP; 6 A; 6 C; 1 G; 1 T; 60 OTHER.
                                                                                                              XXXXXX
                                                                                                                    T 15
PCT-US95-11934-99 STANDARD; DNA; UNC; 75 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 100, Application PC/TUS9511934
Sequence 100, Application PC/TUS9511934
GEMERAL INFORMATION:
APPLICANT: Cytogen Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 1872
REFERENCE/DOCKET NUMBER: 1101-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                 94 AGTCATACCCGGCCCTGTTCCATGTGAGCTGCCAAGGAGGGTCAAGAGGAGGACAAGGGG 35
                                                                                                                                                                       34 CAGCCCA 28
                                                                                                                                                                                              65 NACCACA 71
                                                                                                                                                                                                                                       Match 11.7%;
Local Similarity 7.5%;
es 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Antigen Bir TITLE OF INVENTION: Peptide Fit NUMBER OF COOKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 20-SEP CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
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                                                                                                                                                                                                                                                              Score 21; DB 4; Length 74; Pred. No. 2.73e-01; 19; Mismatches 43; Indels
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Best Local :
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                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) SEQUENCE 75 BP; 1 A; 1 C; 7 G; 5 T; 61 OTHER.
                                                                                           118 AGACTCCTTCAGCTTCAGTTGCAAAGTCATACCCGGCCCTGTTCCATGTGAGCTGCCAAG 59
                                                                                                                                                                                                                                                                       TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 20-SPR-10-1
                                                58 GAGGGT 53
                                                                       64 NNBGGT 69
                                                                                                                                             Match 11.7%;
Local Similarity 7.6%;
les 5; Conservative
                                                                                                                                                                                                                 LENGTH: 75 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                     S. Leslie
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                                                                                                                                             Score 21; DB 4; Ler
Pred. No. 2.73e-01;
18; Mismatches 43;
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	16.7 247 17 AA754458 97SN1784 Rice Immature		
	21.7 252 27 AA754459 97SN1787 Rice Immature 17.2 247 17 AA754458 97SN1784 Rice Immature		ററ
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COMMEN	SUMMARIES		
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REFERE	Mean 9.460; Variance 1.952; scale 4.848	Statistics:	Sta
ACCESS NID VERSIO KEYWOR SOURCE ORGA	:em_est9 7:em_gss1 bank-est111 :gb_est10 10:gb_est11 11:gb_est12 :gb_est1 9:gb_est10 10:gb_est11 11:gb_est12 :gb_est14 14:gb_est15 15:gb_est26 20:gb_est20 :gb_est18 18:gb_est15 19:gb_est23 24:gb_est21 19:gb_est23 24:gb_est21 22:gb_est22 23:gb_est23 24:gb_est21:gb_est23 24:gb_est21:gb_est23 20:gb_est23 24:gb_est23 20:gb_est23 20:gb_est23 20:gb_est3 20:gb_est3 30:gb_est3 31:gb_est4 32:gb_est4 41:gb_gss3 40:gb_gss4 41:gb_gss5 42:gb_gss6	Database:	Dat
RESULT	<pre>emb1-est58 1:em_est10 2:em_est11 3:em_est17 4:em_est18 5:em_est2</pre>	tabase:	Dat
	ng: Minimum Match 0% Listing first 45 summaries	Post-processing:	Pos
C 45	2883791 segs, 1171580779 bases x 2	Searched:	Sea
C 43	: Dbase 0; Query 0	STD	Nmatch
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C 34 C 35 C 37	>US-09-092-296-3 (1-180) from US09092296.seq : 180 1 CAGGAGCGCAGTGGCCACTATTGAAAAGCTCTGCCTCCT 180 GTCCTCGCGTCACCGGTGATGAACTTTTCGAGACGGAGGA	Title: Description: Perfect Score: N.A. Sequence: Comp:	Title: Descri Perfec N.A. S
C C 32	sun OCC 24 17:25:03 1999; MasPar time 365.62 Seconds 1153.579 Million cell updates/sec t not generated.	Tabular output	Tab
	a n.a. database search, using Smith-Wa		MPS
c 23	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	Re1 Cop	
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c 14.			
	李老爷的李爷爷会看他,我们我们的一个女孩,我们就是我们的人,我们就是我们的人,我们就是我们的人,我们就是我们的人,我们就会我们的人,我们就是我们的人,我们就是我们的人,我们就是我们的人,我们就是我们的	* * * * * * * * * * * * * * * * * * * *	*

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4.4 5	43	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
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11.7 11.1	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	•	11.7	•		•			•	•	•	•	•	•
762 37 492 34																							243									
		R61539	ΑIJ	AA59374	AA23996	H4153	AA586	A1522	AA046	A0024376	FRO	T1525	AA275	R3624	T0876	AQ007	W3387	T4741	F1005	M7952	AI382	AA335	D221(B1258	AI063	AQ2357	C2849	W7909	N8055	F0874	040392	B8113
es.≱	orime CK	, ig	EST212268 Normalized r	NCI CO	mw24q07.rl Soares mous	1 Soares	oda - PRL	NCI O	r I	L82 A1 D09 MI	Fugu rubripes GSS segu	lambdaZAPS	.rl Barste	vh91f09_r1_soares_plac	5661 Infant E	CIT-HSP-2292F15.TR CIT	003.rl Soares	£12.	9H122 normali	00065 Mixed stag	qz05f06.x1 NCI_CGAP_CL	9832 E	RICC10342A Rice callus	11-sp6	2	015_B2_C08_T7	93 Rice callus	rl Soares_fe	h06.rl soares fe	ll normalized	2342A Rice shoo	-HSP-2015F16.TFC
1.04e-03 1.55e-02	.04e-	.04e-	.04e-	04e	.04e-	.04e-	.04e-	.04e-	046-	046	.04e-	046	.04e-	046-	046-	.04e-	.04e-	.04e-	.04e-	.04e-	.04e	046	.04e	386	.38e-	. 38e-	.38e-	.38e-	.38e-	.38e-	.38e-	386-

ALIGNMENTS

1 252	source
Location/Qualifiers	FEATURES
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr	
Submitted by Back Hie Nahm, Dept of Biological Science, Myongji	
Email: myeun@sun20,asti.re.kr	
Tel: 82 331 290 0301	
National Inst. of Agri. Sci. and Tech, RDA	
Contact: Eun M.Y.	
On Jan 14, 1998 this sequence version replaced gi:1797457.	COMMENT
Unpublished (1998)	JOURNAL
Large-scale Sequencing Analysis of ESTs from Rice Immature Seed	TITLE
Lee, M.C. and Eun, M.Y.	
Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.,	
Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P.,	AUTHORS
1 (bases 1 to 252)	REFERENCE
Poaceae; Oryza.	
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;	
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
Oryza sativa	ORGANISM
Oryza sativa.	SOURCE
EST.	KEYWORDS
AA754459.1 GI:2801165	VERSION
92801165	NID
AA754459	ACCESSION
cDNA clone 97SN1787, mrNA sequence.	
re Seed Lambda ZAPII cDNA Libr	DEFINITION
AA754459 252 bp mrNA EST 20-JAN-1998	LOCUS
1	RESULT

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SOURCE
ORGANISM
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 CAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 VGNHTRCSRWRBVTRMAH-YHDYTNCBBYNNNDYHMWHBBMYBBTGCMTCTMWCWBHYNT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 BVWYCVASHGNYMSVHNCTBRGTHCDCKNYNWSTMTWGTVNWBNVSGDWHYWBVBNTKVD 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCCTTGACCCTCCTTGG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KCTASGWHTSTNYDVKS-STNTWGVTBSYDKSMHGYWCSBBV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AII36523 328 bp mRNA EST 11-FEB-1999 UI-R-C2p-nq-e-02-0-UI.s1 UI-R-C2p Rattus norvegicus cDNA clone UI-R-C2p-nq-e-02-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                  Email: msoares@blue.weeg.uiowa.edu
The sequence tag present in the cDNA between the NotI site and the
Oligo-dT track served to identify it as a clone from the normalized
adult Lung library. cDNA Library Preparation: M. Fatima Bonaldo,
Ph.D. Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eutheria; Rodentia; Sciurognathi; Murid 1 (bases 1 to 328)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                               Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus
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                                                                                                                                                                                                                                                                           Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 28.3%;
Similarity 12.3%;
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14, 1998 this sequence version replaced gi:1877567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Res. 6 (9), 791-806 (1996)
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/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; Directional cDNA library inserted into lambda ZAPII vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
/organism-"Rattus norvegicus"
/strain-"Sprague-Dawley"
/note-"Wector: pTT3D-Pac (Pharmacia) with a modified
/note-"Wector: pTT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C2p
library is a subtracted library derived from the
UI-R-C0 library. The UI-R-C0 library consisted of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
21 c 12 g 35 t 179 otl
                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="97SN1787"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 51; DB 17;
Pred. No. 9.68e-50;
84; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56; Indels
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ACCESSION KEYWORDS VERSION UID

DEFINITION

δÃ 밁 Ş

148

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BASE COUNT ORIGIN

δÔ 밁

REFERENCE AUTHORS TITLE

JOURNAL MEDLINE

FEATURES

FEATURES

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DEFINITION
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ORIGIN
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Best Local S
Matches 6
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                                  source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 AGGAGGCAGATCTTTTGGAGCATGTCCAGAAAGCCGGAGTCTTGGGAGGTCTTGGCCTGA 269
                                                                                                                                                                                                     Contact: Eun M.Y.
Department of Cytogenetics
National Inst. of Agri. Sci. a
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 252)
Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
Kim,M.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa
Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA754459 252 bp mRNA EST 20-JAN-1998 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza secDNA clone 97SN1787, mRNA sequence.
                                                                                    Email: myeun@sun20.asti.re.kr
Sudmitted by Baek Hie Nahm, Dept of
University, Yongin, Korea. 449-728
Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                             Large-scale Sequencing Analysis of ESTs from Rice Immature Unpublished (1998)
On Jan 14, 1998 this sequence version replaced gi:1797457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.9%;
Similarity 73.6%;
67; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA754459.1 GI:2801165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="UI-R-C2p-nq-e-02-0-UI"
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                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B (Life Technologies)"
77 c 98 g 91 t
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/db_xref="taxon:10116"
/organism="Oryza sativa'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB 23;
Pred. No. 3.33e-36;
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                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                      얁
                                                                                                                                                                                                                                                                                                   Tech,
                                                                                                                       f Biological Science, Myongji
bhnahm@bioserver.myongji.ac.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sativa
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RESULT LOCUS

REFERENCE

AUTHORS

SOURCE VERSION ACCESSION

KEYWORDS

f 밁 ę 밁

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128 MYBBTGCMTCTMWCWBHYNTKCTASGWHTSTNYDVKSSTNTWGVTBSYDKSMHG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 GAAGCTGGACTCATAGGAGGAACTTGTCAGAAAAGACTCCTTCAGCTTCAGTTGCAAAGT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 CATACCCGGCCCTGTTCCATGTGAGCTGCCAAGGAGGGTCAAGAGGAGGACAAG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 VNWBNVSGDWHYWBVBNTKVDVGNHTRCSRWRBVTRWAHYHDYTNCBBYNNNDYHMWHBB 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 8.8%; les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g2801164
AA754458.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                              Department of Cytogenetics
National Inst. of Agri. Sci.
Suwon, Kyunggido, Korea
Tel: 82 331 290 0307
Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nahm.B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P., Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y., Lee,M.C. and Eun,M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA754458 247 bp mRNA EST 20-JAN-199
97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza
cDNA clone 97SN1784, mRNA sequence.
                                                                                                                                                                                                                                                                                                                         Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa.
Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Eun M.Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jan 14, 1998 this sequence version replaced gi:1797455.
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       ρ
                                                                                                                                                 /organism="Oryza sativa"
/cultivar="Milyang23"
/cultivar="Milyang23"
/note="Yector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/note="Yector: pBluescript SK(+); Site_1: EcoRI; Site_2:
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16 c 21 g 34 t 169 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
21 c 12 g 35 t 179 others
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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XhoI; Directional cDNA library inserted into lambda ZAPI
vector at 5'end with BcoRI and 3' end with Xho I Site."
/db_xref="taxon:4530"
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Pred. No. 1.13e-29;
61; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Tech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
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DEFINITION
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REFERENCE AUTHORS

JOURNAL

9

BASE COUNT

FEATURES

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VERSION ACCESSION ç В ဌ В

BASE COUNT

Best Loc Matches

Query Match

DEFINITION RESULT

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Query Match 17.2%;
Best Local Similarity 8.3%;
Matches 11; Conservative
111 SNSVVYVWBTAYCDYBHYBDRANHVDDTRCTNDRGYCNYTASDNGTSATKRVTGYDXTDS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 KRVTGYDKTDSDCGGGCWRKVTYGSSBYBRCGVNVMVRTTSMWTDKSTKMBSM-DMSRRS 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 VNVHSGWNNRCSNSVVYVWBTAYCDYBHYBDRANHVDDTRCTNDRGYCNYTASDNGTSAT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 CAGAGCTTTTCAAGCAATTCCAGGAAGCTGGACTCATAGGAGGAACTTGTCAGAAAAGAC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTCAAGAGGAGG 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVHYGRWMBNKKR 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCTTCAGCTTCAGTTGCAAAGT-CATACCCGGCCCTGTTCCATGTGAGCTGCCAAGGAG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Cytogenetics National Inst. of Agri. Sci. Suvon, Kyunggido, Korea Tei: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae;
euphyllophytes; Spermatoph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g2801164
AA754458.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted by Back Hie Nahm, Dept of Biological Science, Myongji University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
On Jan 14, 1998 this sequence version replaced gi:1797455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 247)
Nahm, B.H., Kim, J.K., Cheong, J.J., kim, S.I., Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., S. Lee, M.C. and Eun, M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA754458 247 bp mRNA EST 20-JAN-1998 97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: myeun@sun20.asti.re.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Eun M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA clone 97SN1784,
                                                                        h 16.7%;
Similarity 9.8%;
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Poaceae; Oryza.
                                                                                                                                                                                                                                                                                                                                                 /Organism="Oryza sativa"
/Cultivar="Milyang23"
/Cultivar="Milyang23"
/note-"vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhOI; Directional CDNA library inserted into lambda ZAPI:
vector at 5'end with EcoRI and 3' end with XhO I site."
/db_xref="taxon:4530"
                                                                                                                                                                                             /clone_lib-"Rice Immature Seed Lambda ZAPII
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host-"E. coli SOLR"
16 c 21 g 34 t 169 others
                                                                                                                                                                                                                                                                                                                    /clone="97SN1784"
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                                                                        Score 30;
Pred. No.
64; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
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Pred. No. 2.88e-17;
71; Mismatches 49;
                                                                           Mismatches
                                                              , DB 17; Lem
, 8.54e-16;
--hes 55;
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                                                                                                                    Length 247;
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Xho I site."
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                                                                                                                                                                                                                                                                                                           85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DCGGGCWRKYTYGSSBYBRCGVNVMVRTTSMWTDKSTKMBSMDMSRRSRVHYGRWMBNKK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGCCCCTTGTCCTCCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATG
                                                                                                                                                                                                                                                                                                         CGGCCCTGTTCCA 73
                                                                                                                                                    AF034173 2275 bp mRNA EST 30-MAR-1998 AF034173 Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA clone ntcon2 contig, mRNA sequence.
AF034173 g2707735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2275)

Tripodis,N. and Ragoussis,J.

Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guys Hospital
7th floor, Guy's Tower, London SEl 9RT, UK
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 275)
Tripodis,N. and Ragoussis,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Tripodis, Nikos
Division of Medical and Molecular Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       boundary
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: nikos@nki.nl
                                                                                                                                    ĀF034173.1 GI:2707735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jan 19, 1998 this sequence version replaced gi:2045115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      438
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cione="ntcon2 contig"
/cione_lib="Human mRNA (Tripodis and Ragoussis)"
, 619 c 470 g 599 t 149 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="6p21.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 28; DB 20; Length 2275; Pred. No. 6.48e-13; 44; Mismatches 19; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2275;
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Best Local Similarity 17.8%;
Matches 19; Conservative
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                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazock; R. G., Fuldner, R. A., Radams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R. A., Ghams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R. A., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R. A., Cline, T. R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N. S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P. S., Jr., Kelley, J.C., Liu, L.-I., Marmaros, S. M., Merrick, J. M., Moreno-Palanques, R. F., McDonald, L. A., Nguyen, D. T., Pelligrino, S. M., Moreno-Palanques, R. F., McDonald, L. A., Nguyen, D. T., Pelligrino, S. M., Moreno-Palanques, R. F., McDonald, L. A., Nguyen, D. T., Pelligrino, S. M., Smilley, R., Small, K.V., Spriggs, T. A., Utterback, T. R., Weidman, J. F., Li, Y., Bednarik, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J., Dimke, D., Feng, D. F., Ferrie, A., Fischer, C., Hastings, G. A., Dimke, D., Feng, D. F., Ferrie, A., Fischer, C., Hastings, G. A., Kozak, D. L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Olsen, H., Raymond, L., Wal, Y. F., Wing, J., Li, H., Meissner, P. S., Olsen, H., Raymond, L., Wal, Y. F., Wing, J., Xu, C., Yu, G. L., Ruber, S. M., Pischer, C., Haseltine, W. A., Fields, C., Fraser, C. M., and Venter, J. C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
AL Nature 377 (6547 Suppl.), 3-174 (1955)

On Apr 14, 1993 this sequence version replaced gi:693635.
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Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2045115
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Division of Medical and Molecular Genetics
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Contact: Kerlavage,
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Cerebellum II Homo
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/db_xref="taxon:9606"
/map="6p21.3"
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/clone_lib="Human mRNA (Tripodis and Ragoussis)"
619 c 470 g 599 t 149 others
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Pred. No. 1.64e-11;
53; Mismatches 33;
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The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA

Bioinformatics

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Eukkaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 459)

Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba;T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA475002 459 bp mRNA EST 18-JUN-1997 vh08h04.r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone IMAGE:874903 5' similar to TR:G466574 G466574 THERMOSTABLE DNA POLYMERASE I ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgl/hgl.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                          WashU-HHMI Mouse EST Project Washington University School of Medicinep 4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1996;
On Jan 25, 1995 t)
                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-HHMI Mouse EST Project
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llarity 89.7%;
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/Organism="Homo sapiens"
/Organism="Homo sapiens"
/Onote="Organ: brain; Vector: pBluescript SK-; Site_1:
CORI; Site_2: XhoI"
/db_xref="ARCC (inhost):124516"
/db_xref="taxon:9606"
/clone_lib="Cerebellum II"
/tissue_type="cerebellum"
/dev_stage="adult"
/dev_stage="adult"
/dev_stage="adult"
/4 g 64 t 4 others
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                   STCMTHYNCCDCKTCGSAGVTVNHHDWSMAGGA 473: | : : : : | | : | : : : : : | | | |
                                                                      GGGTCTGGGCTGCCCTTGTCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGG
GCCGGGTATGACTTTGCAACTGAAGCTGAAGGA 114
                                                                                                                                                                                                                                                                                                                                                                                                               Guys Hospital
7th floor, Guy's Tower, London
Email: nikos@nki.nl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tripodis, N. and Ragoussis, J. Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
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AF038250 Human mRNA (Tripodis
Clone ntcon9, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Tripodis, Nikos
Division of Medical and Molecular Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Jan 19, 1998 this sequence version replaced gi:2045085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
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1 (bassa 1 to 1287)
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219 c 293 g 361 t 65 others
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/db_xref="taxon:9606"
/map="6p21.3"
/clone="ntcon9"
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1. .1287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
iii c 101 g 123 t
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/clone="TMAGE:874903"
/clone_lib="Soares mouse mammary
/sex="male"
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Pred. No. 3.57e-06;
32; Mismatches 37
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Ragoussis) Homo sapiens cDNA
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                                                                                                                                                                                                                                                                                                                               GCTTCCTGGAATTTCTTGAAAATCGCTG 86
                                                                                                                                                                                                                                                                                                                  GCTTCCTGGAATTGCTTGAAAAGCTCTG 174
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B81136.1
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RICS2342A Rice 0
D40392
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   Contact:
National
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mdadams@tigr.org
Clones are available from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
                                        Posceae; Oryza.

1 (bases 1 of 308)
Sasaki, T., Miyao, A. and Yamamoto, K.
Rice cDNA from callus 1995
Unpublished (1995)
                                                                                                                    Oryza sativa.
Oryza sativa
Chyza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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                                                                                                                                                                                             g569543
D40392.1 GI:569543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   end search page:
http://www.tlgr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21
Class: BAC ends.
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1 (bases 1 to 259)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/clone="2015F16"
/clone_lib="CIT-HSP"
/sex="Male"
Takuji Sasaki
Institute of Agrobiological Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HindIII"
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43 c 56 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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e shoot
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Pred. No. 6.38e-05;
0; Mismatches 3
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Oryza sativa cDNA, mRNA sequence.
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115 GCTGCACCTCCTCCTCCTCCTCCTCCTCAGGAGCTCCAATGGA 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 339)

Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Juneau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.

Sebastiani-Kabaktchis,C. and Tessier,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: tsasaki@abr.affrc.go.jp.
Location/Qualifiers
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Fax: 0298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 331697/2800
Fax: 33160778698
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HSC1DB011 normalized infant brain
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                                                                                                                                                                                                                                                                                                                                                                                                                Email: genexpress@genethon.fr
Single read.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genexpress-Genethon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Genethon
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llarity 73.9%;
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/organism="Homo sapiens"
/organism="Homo sapiens"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
/note="Organ: brain; Vector: lafmid BA; Site_2: NOTI:
Site_2: NOTI: sex=Female; dev_stage=3 months old;
Site_2: NotI: sex=Female; dev_stage=3 months old;
Site_2: NotI: sex=Female; dev_stage=3 months old;
Isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dT) primed and directionally
Cloned 5. - 3. into the HindIII -> NotI sites of the
lafmid BA vector: Clone library from B.Soares, psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, p.N.A.S in press"
/db_xref="taxon:9606"
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/strain="Nipponbare, sub_species Japonica"
/note="Etiolated shoot (8 days old)"
/db_xref="taxon:4530"
/clone_lib="Rice shoot"
1 126 c 57 g 68 t
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Pred. No. 6.38e-05;
0; Mismatches 12
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Matches 43; Conser
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 314 286 1800 Email: est@w===
                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: reverse ET
High quality sequence executive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 427)
Hillier.L., Clark.N., Dubuque.T., Elliston.K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing.T., Soares,M., Tan,F., Trevaskis,E., Waterston.R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N80550 427 bp mRNA EST 02-APR-1996 zal0h06.rl Soares fetal liver spleen 1NFLS HDmo sapiens cDNA clone IMAGE:292187 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
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Location/Qualifiers
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ilarity 66.2%;
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                  /sex="male"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/lab_nost="107 g 84 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="normalized infant brain cDNA"
/sex="Female"
/tissue_type="total brain"
/dev_stage="3 mDnths old"
116 c 100 g 64 t 2 others
                                                                                                      /clone_lib="Soares fetal liver spleen lNFLS"
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 AACTTGATGGAAAAGANTGCTTCAGCCTTNGTTGGACCGGCAAGCCCG 298
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Local Similarity 70.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases I to 433)

1 (bases I to 433)

1 (bases, To 433)

1 (bases, To 434)

2 (bases, To 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 826 Std Error: 0.00
Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1995)
Dn May 8, 1995 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson, R.
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Zd75h10.rl Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
IMAGE:346531 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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Location/Qualifiers
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                                                                                                                                                                   /clone_lib="Soares_fetal_heart_NbHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/lab_host="DH10B (a mpicillin resistant)"
                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE: 346531"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NbHL19W
                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GDB:1271906"
/db_xref="taxon:9606"
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                                                  12.2%;
                                                  Score 22; DB 34;
Pred. No. 6.38e-05;
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Pred. No. 6.38e-05;
0; Mismatches 14
                    Mismatches
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                    10;
                                                                              Length 433;
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317 CCCCTTCCCTCCTCCAGACCCTCCTTGGCCGGTGACNTNG 356

Qy 36 CCCTTGTCCTCCTTGACCCTCCTTGGCAGCTCACATGG 75

Search completed: Sun Oct 24 17:32:17 1999 Job time : $374\ \text{secs}.$

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Fri Oct 22 18:41:27 1999; MasPar time 5.65 Seconds 293.555 Million cell updates/sec

Description: Perfect Score: Tabular output not generated. >US-09-092-296-15 (1-78) from US09092296.pep 558 1 MGSGLPLVLLLTLLGSSHGT......SGTSVTLHHARSQHHVVCNT 78

Scoring table: PAM 150 Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

i:parti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38 39:part39

Statistics: Mean 27.329; Variance 130.705; scale 0.209

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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R66060	R06110	R10052	R15138	W10040	W10038	W59924	W21674	R26954	W57046	R47338	R48730	W02702	W73408	W70327	W88498		3
Human NMDAR2 receptor	Sequence of cyclomalt	Cyclomaltodextrin glu	Human serotonin lD re	Mad binding protein,	Mad binding protein,	Human 7-transmembrane	Human mitochondrial e	Human T lymphocyte re	Mouse apoptosis induc	Peptide fragment of t	G-protein coupled bov	G-protein coupled bov	Human secreted protei	Secreted protein FB78	Human stomach carcino	neact Thereon	
9.93e+01	9.93e+01	9.93e+01	9.93e+01	8.50e+01	8.50e+01	8.50e+01	7.28e+01	7.28e+01	6.23e+01	6.23e+01	4.56e+01	4.56e+01	3.89e+01	3.89e+01	2.84e-38	Fred. No.	

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Human	Lipopo	Recombinant	Mouse	snbR ç	Glutamic	C-Delt	C-Delt	Kaposi	Kaposi	Human	_		Human	Human	Amino	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human
ke	o	inant endotoxin	EI24 protein	gene product inv		1 polypept	ta-1 polypeptide	's sarcoma a	s sarcoma a	secreted protei	protein tyrosin	I diabetes-assoc	n3	sulinoma-ass	id :	c-Fos induced q	NMDAR2 receptor	v1-D-a	œ .	Ö	e e	N-methy1-D-aspa	NMDAR2 receptor	1-D-as	N-methyl-D-aspa		_	N-methyl-D-aspa
⊥.8	1.8	1.83	1.83e		1.3	1.35	<u>س</u> د :	1:3	1.3	- 1	1.16	1.1		_	Ŀ		9.93e+0	9	9	۰	9	9.9	9	9.93	9.9	9.93€	9.93e+	9.936

ALIGNMENTS

		PI rarge-Scale protest PS Claim 1; Page 135; CC This is the amino CC encoded by human s CC The encoded nrotest			SUL
9 G . B B	internal transmembrane domain. The invention provides nucleotide sequences (see V8439-75) coding for 18 transmembrane proteins sequences (see V8439-75) coding for 18 transmembrane proteins (see W88491-508), vectors containing such polynucleotides, and eukaryotic cells containing the vectors. The proteins can be	Larye-scale procein production, gene diagnosis, and gene therapy Claim 1; Page 135; 178pp; English. This is the amino acid sequence of a novel transmembrane protein encoded by human stomach cancer cDNA clone HP10408 (see V84356). The encoded by notein has a nuttitive storal conventions are	WPI; 99-045730/04. N-PSDB; V84366. New human proteins containing transmembrane domains and their encoding sequences – useful in the preparation of antibodies and	45. 44948. 7 INC. 1EM RES CENTRE. Yamaguchi T;	w8498 standard; Protein; 78 AA. W88498; 30-MAR-1999 (first entry) Human stomach carcinoma HP10408-encoded transmembrane protein. Transmembrane protein; HP10408; human; stomach cancer.

Score 558; DB 39; Length 78; Pred. No. 2.84e-38; 0; Mismatches 0; Indels

Indels 0;

Gaps

0

B

Query Match 100.0%; Best Local Similarity 100.0%; Matches 78; Conservative

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RESULT
1D W
AC W
DT H
DE H
CKW S
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Probleman form human foetal kidney, adult colon, adult brain, foetal probleman foetal kidney, adult colon, adult brain, foetal from and placenta colon brain secreted protein consistency. It is the amino acid sequence of novel human secreted protein consistency. This is the amino acid sequence of novel human secreted protein searching revealed some similarity between f8781 and some known consequences. The invention provides new isolated polynucleotides sequences. The invention provides new isolated polynucleotides (see V33190-99), from human foetal kidney, adult colon, adult brain, confects foetal brain and placenta cDNA libraries, that code for secreted production of the polypeptides, which may have activities such as production of the polypeptides, which may have activities such as a production activity, cytokine and cell proliferation or differentiation activity, which may have activity, activing themselves activity, tissue growth activity, activing activity, themselves activity, receptor/ligand activity, antional activity, condherin/tumour invasion suppressor activity, tumour inhibition activity, or other activities.
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Best Local S
Matches 1
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24-FEB-1998; US-028724.
26-FEB-1998; US-028724.
26-FEB-1998; US-028724.
26-FEB-1998; US-028724.
(GEMY ) GENETICS INST INC.
AGOSTINO MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg Racie LA, Spaulding V, Treacy M;
WPI; 98-481139/41.
                                                Human secreted protein encoded by Gene No. 12. Secreted protein; human; protein therapy; gene therapy; blood disorder; pathological condition; diagnosis; cancer; neurological disorder; developmental abnormality; foetal deficiency; leukaemia; hepatic disease; immune system disorder; Alzheimer's disease; cognitive disorder; schizophrenia; prostate disease; autoimmune disorder; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 98-481139
N-PSDB; V33199
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Secreted protein; DU123_1; human.
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W70327 standard; Protein; 46 AA.
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  Misc_difterence
                                    Homo sapiens.
                                                                                                                                                                                                        W73408 standard;
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2 GSGLP-LVLLTTLLGSSHGTGPG
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Similarity 56.5%;
13; Conserved
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Pred. No. 3.
6; Mismatc
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+ches 3; Indels
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PT New isolated human genes: useful for diagnosis and treatment of, PT e.g. cancers, neurological disorders, immune diseases, developmentai PT disorders or biood disorders
PS Claim II; Page 152-153; 188pp; English.
CC This sequence is encoded by a cDNA of the invention, designated Gene No. 12. This sequence represents a human secreted protein, and is CC expressed in activated neutorphils, endothedial cells, T-cells and CC to a lesser extent in brain and liver. The DNA sequences of the invention and their corresponding secreted CC polypeptides are useful for preventing, treating or ameliorating medical CC conditions, e.g. by protein or gene therapy. Also pathological conditions CC can be diagnosed by determining the amount of the new polypeptides in a CC sample or by determining the presence of mutations in the DNA sequences. Specific uses are described for each of the DNA sequences and the encoded CC proteins, based on which tissues they are most highly expressed in, and CC include developing products for the diagnosis or treatment of cancer, CC deficiencies, blood disorders, developmental abnormalities and foetal CC deficiencies, blood disorders, leukaemias, diseases of the immune system CC including allargies or asthma), hepatic disease, Alzheimer's and CC disorders and AIDS. The polypeptides are also useful for identifying CC sequence 47 AA;
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Matches 1
                                                                    US5508384-A.
16-APR-1996.
10-SEP-1992; 943236.
10-SEP-1992; US-943236.
09-SEP-1993; US-118270.
(UTNY ) UNIV NEW YORK STATE.
MUTPHY RB, Schuster DI;
WPI; 96-208785/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-MAY-1998; U10868.
29-AUG-1997; US-056296.
30-MAY-1997; US-044039.
30-MAY-1997; US-048093.
30-MAY-1997; US-048190.
30-MAY-1997; US-048190.
30-MAY-1997; US-048196.
30-MAY-1997; US-048356.
30-MAY-1997; US-056250.
29-AUG-1997; US-056250.
                                                                                                                                                                                                                                                         G-protein coupled bowine adrenal angiotensin II type-1 receptor. G-protein coupled receptor; ligand binding assay; transmembrane domain; schizophrenia; oppanine; cAMP; adenosine; thrombin; adrenergic; opsin; muscarinic acetyicholine; endothelin; bombesin; endocrine; rhodopsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carter KC, Dillon PJ, Rosen CA, Ruben SM, Yo
New dopamine receptor peptide - useful as antipsychotic agent, e.g. for treating schizophrenia Disclosure; Column 129-132; 184pp; English. Proteins w02657-W02730 represent a range of G-protein coupled receptor
                                                                                                                                                                                                                                             odorant;
                                                                                                                                                                                                                                                                                                                                                                          w02702 standard; peptide; 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 99-070209/06.
N-PSDB; V08822.
                                                                                                                                                                                                                                                                                                                                                          W02702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
Carter KC, Dillon PJ, Endress
                                                                                                                                                                                                                                                                                                                                      13-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               6 gaalpiillllalrgtfhgarpg 28
|::|| |:|||:| |: ||: ||
2 GSGLP-LVLLLTLLGSSHGTGPG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
13; Conse
                                                                                                                                                                                                                                             cytomegalovirus; serotonergic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.4%;
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Pred. No. 3.89e+01;
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RESULT
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AC R.
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Best Local
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17-MAR-1994.
09-SEP-1993; U08528.
10-SEP-1992; US-943236.
(UYNY ) UNIV NEW YORK STATE.
MUZDBY RB, Schuter DI;
WPI; 94-101120/12.
  R47338 standard; Protein; 194 AA.
R47338;
01-JUL-1994 (first entry)
Peptide fragment of tetracycline transporter protein.
Peptide fragment transport protein; gene therapy; screening vesicle membrane transport protein; dentification; detection;
Parkinsons disease; neurotoxin; identification; detection;
Parkinsons disease; neurotoxin; identification; detection;
                                                                                                                                                                                                                                                                                                                                                                adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin, odorant, cytomegaloviral and other G-protein coupled receptors. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand binding assays. The polypeptide fragments retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see R48759-R48758, R50569-R50807 and R89189-R89195 for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptides of G-coupled receptor proteins (GPRs) - useful for binding GPR ligands or modulating GPR binding Disclosure; Page 106-107; 160pp; English.

Proteins R48685-R48758 represent a range of G-protein coupled receptor proteins selected from CAMP, adenosine, muscarinic acetyloboline, in the coupled receptor proteins selected from CAMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G-protein coupled bovine adrenal angiotensin II type-1 receptor protein. G-protein coupled receptor; ligand binding assay; transmembrane domain; psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin; muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine, addrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin, odorant, cytomegaloviral and other GPR proteins. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand binding assays. The polypeptide fragments retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see W02747-W0299) for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rhodopsin; opsin;
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                                                                                                                                                                                                                                        27 ymklktyasvfllnlaladlcflltlp
                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 FITNSSYESSEL-EL-LEKLCLLLHLP 58
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                                                                                                                                                                                                         FLINSSYESSFL-EL-LEKLCLLHLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in 15.2%;
Similarity 44.4%;
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Pred. No. 4.
5; Mismatc
                                                                                                                                                                                                                                                                                Score 85; DB 16;
Pred. No. 4.56e+01;
5; Mismatches 8
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amine transporter protein;
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                                                                                                                                                                                                                                                                                                                          Length 325;
                                       screening;
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PD NA, vectors, transformed cells and antibodies, for diagnosis and treatment of neurological disorders, e.g. Parkinson disease

PT treatment of neurological disorders, e.g. Parkinson disease

PS Example 2: Page 111-112; 181pp: English.

CT his sequence of the tetracycline transporter protein showed a content (CGAT) of rat. The cDNA encoding the chromaffin granule are protein (CGAT) of rat. The cDNA encoding the chromaffin granule can ine transport protein is useful in gene therapy and as a probe complete the compounds implicated in Parkinsons disease, contenting genomic sequences. The transport protein is used for screening cytotoxic compounds implicated in Parkinsons disease, considered with activity of neurotoxins or psychiatric diseases associated with activity of neurotoxins or psychiatric consorders and to identify compounds which selectively inhibit or activate its action. Antibodies raised against the transport protein are useful as immunoassay reagents for detecting the protein as affinity reagents for purification.
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Matches 1
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03-OCT-1997; U17876.
04-OCT-1996; US-044456.
(IMMV) IMMUNEX CORP.
                                                                                                                                      DNA encoding apoptosis inducing receptor - which is Type I transmembrane protein, useful for regulating cell death Claim 16; Page 33-35; 45pg; English.

This sequence is the mouse apoptosis inducing receptor (AIR) of the invention. AIR is a Type I transmembrane protein, soluble forms of which can be used to regulate cell death in a therapeutic setting. Soluble AIR can also be used in vitro to block apoptosis or AIR-expressing cells, or to screen agonists or antagonists of AIR activity. The cytoplasmic domain of AIR can be used to develop assays for inhibitors of AIR-induced cell death, which is useful to regulate cell death in a therapeutic setting as well as in vitro. Agonists of AIR activity can be used to kill tumour cells that express AIR, or T cells expressing AIR in autoimmune diseases. Sequence 411 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-AUG-1998 (first entry)
Mouse apoptosis inducing receptor.
Apoptosis inducing receptor; AIR protein; mouse;
Type I transmembrane protein; tumour cell death;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 98-240077/21.
N-PSDB; V28701.
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WO9814565-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perkins PA;
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11-JUN-1993;
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Local Similarity 31.0%;
nes 18; Conservative
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          . Similarity
12; Conser
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       14.9%;
ilarity 57.1%;
Conservative
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; US-923096.
7 CALIFORNIA.
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       Score 83;
Pred. No.
5; Misma
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Pred. No. 6.23e+01;
13; Mismatches 23;
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DB 31; Le..
6.23e+01;
Thes 3;
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autoimmune disease;
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Matches
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08-FEB-1991; FR-001487.
12-APR-1991; FR-004527.
(ROUS ) ROUSSEL-UCLAF.
Ferradini L, Hercend T, R
WPI: 92-300035/36.
N-PSDB; 028129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA was isolated from peripheral lymphocytes and converted to cDNA. The cDNA was amplified by anchored PCR using C-alpha and polyc primers. The amplified again using a different C-alpha specific primer. The amplified grain using a different C-alpha specific primer. The amplified product was SacII-restricted, inserted into Bluescript SK+ vector and used to transform E.cocli XI7-blue. Transformants were screened with a C-alpha specific probe and DNA from positive clones was sequenced in the C-alpha region. The sequence designated "IGR a 12" comprises the complete coding region of a gene of the subfamily v alpha 22; this subfamily was previously identified by the partial sequence (113bp) AC9 (Klein, M.H., et al., Proc.Natl.Acad.Sci. USA 84:6884, 1987). The peptide encoded by It can be used to block specific T cell epitopes or in vaccines.
New mammalian artificial chromosomes - comprising a mammalian centromere and a unique cloning site, used for stable expression product of the CII-3 gene identified in mammalian artificial chromosome MAC-8.2.3, which is contained in the human-hamster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human T-lymphocyte
for therapy
Claim 8; Page 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequences and their monoclonal antibodies and oligo:nucleotide primers - encode variable alpha-chain regions human T-lymphocyte receptors, for studying immune responses and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ното
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29-OCT-1996; U17476.
31-OCT-1995; US-550717.
(REGC.) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                          Human mitochondrial electron transport chain subunit CII-3. Mammalian artificial chromosome; MAC; selectable marker; CII-3; mitochondrial electron transport chain complex II.
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R26954;
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N-PSDB; T72466.
                                                                                                                                                              Scheffler IE;
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W21674;
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                                                                                                                                                                                                                                                                                                                          29-SEP-1997 (first entry)
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MGSGLPLV-LLLTLLGSSHGTG-PGMTLQLKLKE-SELT-NSSY-ESSFLELL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subtype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1ymphocyte receptor V-alpha22 segment.
R a 12; variable region; immune system modulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.7%;
llarity 34.0%;
Conservative
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Pred.
12; M
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    comprising a mammalian
used for stable expression

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28e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
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                                                                                                                                                                                  by HIV 1 or 2.

Claim 1; Page 18-19; 24pp; English.

C This polypeptide comprises HNPDY20, a novel human 7-transmembrane

C G-protein coupled receptor that shows about 30.8% identity in 299

C amino acid residues with the thrombin receptor. Its amino acid

c sequence was deduced from an isolated HNPDY20 polynucleotide

C sequence (see V53631). The invention relates to HNPDY20

C polypeptides and recombinant materials and methods for their

C production. It also provides methods for using such polypeptides

C and HNPDY20 polynucleotides for treatment of infections such as

C bacterial, fungal, protozoan and particularly HIV-1 or HIV-2

C bacterial, fungal, protozoan and particularly HIV-1 or HIV-2

C bacterial, fungal, protozoan and particularly HIV-1 or HIV-2

C bacterial, fungal, protozoan and particularly HIV-1 or HIV-2

C bacterial, fungal, protozoan and particularly HIV-1 or HIV-2

C bacterial, fungal, protozoan and particularly HIV-1 or HIV-2

C bacterial, fungal, protozoan and particularly HIV-1 or HIV-2

C bacterial, fungal, protozoan and particularly macrosis, including asthman, Parkinson's disease, acute heart failure, hypotension,

C mycertension, urinary retention, osteoporosis, angina pectoris,

C mycertrophy, and psychotic and neurological disorders, including

C anxiety, schizophrenia, manic depression, delirium, dementia,

Severe mental retardation and dyskinesias, such as Huntingdon's

severe mental retardation and dyskinesias, such as Huntingdon's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP.
Bergsma DJ, Fuetterer WS, Mao JY, Sathe WPI; 98-482962/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human 7-transmembrane receptor HNFDY20.

HNFDY20; G-protein coupled receptor; human; infection; HIV; pain; cancer; anorexia: asthma: Parkinson's disease; acute heart fallure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; ulcer; allergy; benign perstatic hypertrophy; psychosis; anxiety; schizophrenia; manic depression; delirium; dementia; mental retardation; dyskinesia; Huntingdon's disease; Gilles de la Tourette's syndrome; dyskinesia; Huntingdon's disease; Gilles de la Tourette's syndrome;
                  disease or Gilles de la Touretté's syndrome. Gene therapy using RNA encoding HNYDY20 can be used to treat conditions caused by under-expression of the protein. The invention also relates to methods of identifying agonists and antagonists and for using such compounds to treat conditions associated with HNYDY20 imbalance. Diagnostic assays for detecting diseases associated with inappropriate HNYDY20 activity or levels are also provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides and polypeptides encoding a novel human 7-transmembrane receptor - useful for diagnosing and treating e.g. cancer, osteoporosis and Parkinson's disease and infections caused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     animals.
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16-FEB-1998; 301122.
19-MAR-1997; US-820521
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  Sequence
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with inappropriate Sequence 401 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 slpmamsichrgtgialsagvsl-fgms-alllpgnfes-ylelvkslcl:||::::|:::||::||::||::||::||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 GLPLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLCL
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. 7.28e+01
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eart failure;
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Query Match Best Local S Matches

Similarity 8; Conser

14.5%; ilarity 38.1%; Conservative

Score 81; DB 35; Pred. No. 8.50e+01 9; Mismatches

Length 401; Indels

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Gaps

δõ

34

332

W10038;

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PT msin nucleic acids encoding recombinant polypeptide(s) that
PT associate with Mad polypeptide - are possible homologues of S.
PT cerevisiae general repressor protein Sin Sin Sequence 12; Fig 23A-C; 1llpp; English.

PT cerevisiae general repressor protein Sin Sin Sequence represents the murine protein, designated msinA, which may complex english.

CT his sequence represents the murine protein, designated msinA, which may complex english associates with a Mad complex which preferably associates complex which preferably associates are polypeptide to form a msin:Mad.Max complex which binds to a completide sequence comprising CACGTG. Mad is a basic helix-loop-helix complex super protein which can compete with Myc by forming sequence complexes activate, transcription from promoters containing colored protein complexes with Max. Mad:Max complexes repress, while Myc.Max complexes activate, transcription from promoters containing colored protein captured to differentation in at least two distinct cell lineages. The switch from Myc.Max to Mad:Max complexes may reflect the repression contains useful in elucidation of Mad repressor functions.

SQ Sequence 1253 AA;
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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29-APR-1997
01-JUN-1994; 252966.
01-JUN-1994; US-552966.
19-SEP-1991; US-756195.
23-JUN-1992; US-903710.
01-APR-1994; US-222638.
(HUTC-) HUTCHINSON CANCER RES CENT FRED.
Ayer Ds. Elsenman RN;
WPI; 97-258216/23.
N-PSDB; T70126.
  07-FEB-1998 (first entry)
Mad binding protein, mSinA9.
murine; mSinA; mammalian homologue; Saccharomyces cerevisiae; repressor;
Sin3; Mad; Max; mSin:Mad complex; mSin:Mad:Max complex; Myc; promoter;
basic helix-loop-helix zipper protein; compete; DNA-binding;
Myc:Max complex; activate; transcription; gene regulation.
                                                                                                                         T 12
W10040 standard;
W10040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           murine; mSinA; mammalian homologue; Saccharomyces cerevisiae; repressor; Sin3; Mad; Max; mSin:Mad complex; mSin:Mad:Max complex; MyC; promoter; basic helix-loop-helix zipper protein; compete; DNA-binding; MyC:Max complex; activate; transcription; gene regulation.
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W10038 standard; Protein; 1253
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FLINSSYESSFLELLEKLCLL
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Similarity 27.5%;
11; Conservative
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1238
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'note= "encoded by TAG"
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transcription; gene regulation
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Pred.
14; M
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                                                                                                                                                                                                                                                                                                                          DB 25;
8.50e+01;
                                                                                                                                                                                                                                                                                                    14;
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Query Match
Best Local S
Matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide to form a mSin:Mad complex, which preferably associates with a Max polypeptide to form a mSin:Mad complex complex which binds to a nucleotide sequence comprising CACGTG. Mad is a basic helix-loop-helix (BHLH) zipper protein which can compete with Myc by forming sequence-specific DNA-binding heterocomplexes with Max. Mad:Max complexes repress, while Myc:Max complexes activate, transcription from promoters containing proximal CACGTG binding sites for these proteins. Expression of Mad is closely linked to differentation in at least two distinct cell lineages. The switch from Myc:Max to Mad:Max complexes may reflect the repression of transcription of Myc regulated genes by Mad. The DNA, vectors and host cells of the invention are useful for the recombinant production of mSin proteins useful in elucidation of Mad repressor functions.
                                                                                                                                                                                                                                                                                                                          R15138 standard; Protein; 398 AA.
R15138;
R15138;
I7-FEB-1992 (first entry)
Human serotonin 1D receptor encoded by gene 11.
5-HT (1D); Parkinson's Disease; migraine; anxiety; eating disorder;
6-protein; 5-hydroxytryptamine.
                                                                                                                                                                                                                                                                            Key
domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mSin nucleic acids encoding recombinant polypeptide(s) that associate with Mad polypeptide - are possible homologues of cerevisiae general repressor protein Sin3 Example 12; Fig 29A-C; 111pp; English.
                                   domain
                                                                          domain
                                                                                                                domain
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                                                                                                                                                                                               domain
                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the murine protein, designated mSinA9, which may be a mammalian homologue of the Saccharomyces cerevisiae general repressor protein Sin3. The mSin protein associates with a Mad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUTC-) HUTCHINSON CANCER RES CENT
Ayer DE, Eisenman RN;
WPI; 97-258216/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUN-1992; US-903710
01-APR-1994; US-222638
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                                                                                                                                                                                                                                         domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
11; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1261 AA;
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                                                                                                                /label=
111..171
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                                                    /label=
                                                                                                                                                                         label = cytoplasmic
                                                                                                                                                                                                                 /label= transmembrane-1
                                                                                                                                                                                                                                                           /label= extracellular
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                                   164
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             cytoplasmic
                                                       transmembrane-3
                                                                                          extracellular
                                                                                                                                    transmembrane-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 81; DB 25;
Pred. No. 8.50e+01
14; Mismatches 1
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Matches

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NR-PSDB (201835.)

PR N-PSDB (201836.)

PT Nucleic acid encoding 5HT-1D receptors and their antibodies - provided to treat and diagnose conditions caused by abnormal 5HT-1D receptor expression e.g. dementia proceptor encoded by gene 8-30-84 cc and gene 11, respectively. A full-length clone corresponding to and gene 11, respectively. A full-length clone corresponding to gene 11 was isolated from a human placental library. The cc amino acid sequence deduced from the nucleotide sequence predicts a mol.wt. 44,333 protein. Comparison of this protein sequence with previously characterised neurotransmitter receptors suggests that it is a new_member_of, the G protein-coupled receptor family.
 PRATER TO PARE CLL
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Best Local S
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08-MAY-1991; U03200.
08-MAY-1990; US-520716.
(NEUR-) NEUROGENETIC CORP.
Weinshank RL, Branchek T, Hartig P
WPI; 91-353715/48.
J02286080-A.
26-NOV-1990.
28-APR-1989;
                                          region
                                                                                                                                  peptide
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                                                                                                                                                                                                      Cyclomaltodextrin
                                                                                                                                                                                                                               R10052 standard; Protein; 713 R10052;
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                                                                                                                                                                                                                   19-MAR-1991
                                                                                                                                                                                                                                                                                                                                             66 HHARSQHHVVCN 77
                                                                                                                                                                                                                                                                                                                                 LVLLLTLLGSSHGTGPGMTLQLKLKESFL-TNSSYESSFLELLEKLCLLLHLPSGTSVTL 65
                                                                                                                                                                                                                                                                                                         tdrwtlsqvvcd 123
                                                                                                                                                                                                                                                                                                                                                                              Similarity
17; Conser
                                                                                                                                                                                 strain
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398 AA;
                                                                                                                                                                                                 (first entry)
extrin glucotransferase 17-1.
                                                                                                                                                                                                                                                                                                                                                                           14.3%;
ilarity 23.6%;
Conservative
 110603
                                           /label=
206..229
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189..205
                                                                                        /label- U1
261..439
                                                                                                                                   /label- signal peptide 28..44
                                                                                                                                                                                17-1 (ATCC 31007)
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373..398
                                                                                                                         /note= "confirmed by N-terminal Edman degradation"
                                                                                                                                                                     Location/Qualifiers
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339
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Pred. No. 9.
22; Mismatc
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9.93e+01;
9.3 32;
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Search completed: Fri Job time : 55 secs.

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RESCRIPTION OF SECOND S
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Best Local S
Matches 1
                                                                                                                          Matches
                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                              Cyclo:malto:dextrin glucano:transferase coding DNA sequence -
including corresp, plasmid and microbe transformed by plasmid
Disclosure; Page 831; 16pp; Japanese.
DNA, the plasmid contg, it, and any microorganism transformed with the
plasmid are new. Transformed strains show CGTase activity after 16 hrs
culture on LB plate. 38-2 CGTase and 17-1 CGTase genes are each stably
retained in E.coli cells translated to CGTase efficiently. Large amts.
polypeptide with CGTase activity can be obtd.
Sequence 713 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coding amino acid sequence.

Disclosure; Fig 6; 16pp; Japanese.

The sequence is deduced from a DNA from pUCP1. The sequence is divided into four units (U1-U4) by restriction sites in the DNA. By combining these with similar units (S1-S4) from CGTase 38-2 (R10051), e.g.S1-U2-U3-S4 or U1-S2-U3-S4. enzymes with properties of both strains can be produced. The hybrids compensate for defects in the individual enzymes and can be designed to display optimum characteristics of pH and temperature stability. See also R10052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-APR-1989; JP-110603
(RIKA) RIKAGAKU KENKYUSHO.
WPI; 91-012216/02.
Q-PSDB; Q10164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JAN-1990.
28-MAR-1988; 105945.
10-JUL-1987; JP-172722.
8-MAR-1988; JP-105945.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RIKA) Rikagaku Kenkyusho.
WPI; 90-047991/07.
N-PSDB; Q01810.
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Sequence of cyclomaltodextrin glucanotransferase (CGTase)
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                                                                                                                          h 14.3%;
Similarity 34.2%;
13; Conservative
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larity 34.2%;
Conservative
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                                                                                                                       Score 80; DB 1; L
Pred. No. 9.93e+01;
14; Mismatches 8
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Pred. No. 9.93e+01
14; Mismatches
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Fri Oct 22 18:45:15 1999; MasPar time 2.38 Seconds 383.184 Million cell updates/sec

Tabular output not generated.

Scoring table: Description: Perfect Score: PAM 150 Gap 11 >US-09-092-296-15 (1-78) from US09092296.pep 558 1 MGSGLPLVLLLTLLGSSHGT.....SGTSVTLHHARSQHHVVCNT 78

Searched: 119857 seqs, 11713122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 25.509; Variance 122.762; scale 0.208

SUMMARIES

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120	429	1244	1239	1236	1231	1219	1214	398	398	390	390	390	390	169	1261	1253	401	169	194	194	325	325	Length	
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29,	ω u	•	52,	6, 2	48,	`	54,	6	6	ζ,	6	ζ,	Sequence 6, Appl	4,	18,	12,	,2	'n	%	œ	51,	Sequence 51, App	Description	
Applicati	1102+3	Applicati	licati	icatio	Applicati	Applicati	Applicati	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicati	Applicati	Applicatio	Applicatio	Applicatio	Applicatio	Applicati	licati		
6.06e+01			•		4.43e+01	4.43e+01	4.43e+01	4.43e+01	٠		4.43e+01		4.43e+01	4.43e+01	3.78e+01	3.78e+01	3.78e+01	3.23e+01	2.75e+01	2.75e+01	2.00e+01	2.00e+01	Pred. No.	

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Pecque Set Quality	25 25 26 27 28 29 29 29 30 31 31 31 31 31 31 31 31 31 31 31 31 31
Sequence 51, Patent No. 5: GENERAL INFORMATION OF TELEPAX TELERAL TO SEQUENCE (STREET) STREET: COUNTY: VIPE COMPUTER INFORMATION APPLICAN FILING I ATTORNEY, AREAUTH SOFTWARE APPLICAN FILING I ATTORNEY, AREAUTH TELEPAX TELECOMMUTELE TELECOMMUTE IN SOFTWARE APPLICAN FILING I ATTORNEY, AREAUTH TELECOMMUTE IN SOFTWARE APPLICAN FILING I ATTORNEY, AREAUTH AREAUTH TELECOMMUTEL	CC 11 7706 Ce 11 7766 7766 7766 7766 7766 7766
5 App 5 ORMA 6 O	70.
equence 51, Application US/0811 atent No. 5508384 GENERAL INFORMATION: APPLICANT: SCHUSter, David I TITLE OF INVENTION: RECEPTOR NUMBER OF SEQUENCES: 348 CORRESPONDENCE ADDRESS: ADDRESSEE: BROWDY AND NEIM STREET: 419 Seventh Street CITY: Washington STREET: D.C. COUNTRY: USA ZIP: 20004 COMPUTER READABLE FORM. MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatibl OPERATING SYSTEM: PC-DOS/M SOFTWARE: Patentin Release CURRENT APPLICATION NUMBER: US/08/ FILING DATE: 10-SEP-1993 PRIOR APPLICATION NUMBER: US/08/ FILING DATE: 10-SEP-1993 PRIOR APPLICATION NUMBER: 34,03 REFERENCE/DOCKET NUMBER: M TELECOMMUNICATION INFORMATION NAME: TOWNSONIA, Kevin G. REGISTRATION NUMBER: 34,03 REFERENCE/DOCKET NUMBER: M TELECOMMUNICATION INFORMATION TELEPAX: 248633 TELEPAX: 248633 TELEPAX: 248633 TELEPAT: 335 anino acids TYPE: amino acids	S 8111111111177770877790
. Randal . Randal . Randal . Randal . RAND . ROLLE . ROLLE . RECEE . Dy AND N . DN . AND N . DN . AND N . DN	US PPUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU
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F G-COUPLED P COMPOSITIONS , Suite 300 Version #1.2	Sequence Seq
FIONS #1.25	11 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
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Best Local Similarity 44.48;
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TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE 325 AA; 37288 MW; 592694 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XXXXXX
                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 51, Application PC/TUS9308528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCI-US93-08528-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 51, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SPOTEMBER: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 FLINSSYESSFL-EL-LEKICULLHIP 58
  34
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                         27
                                                                                                                                                                        TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATE: 05 07/943,236
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ANTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                          MOLECULE TYPE: peptide
JENCE 325 AA; 37288 MW; 592694 CN;
                                                                                                                                                              SEQUENCE CHARACIERISTICS
                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                YMKLKTYASVFLLNLALADLCFLLTLP 53
  FLTNSSYESSFL-EL-LEKLCLLLHLP 58
                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Wa
STATE: D
COUNTRY:
                                                                                                                                                                                                                                NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2
                                                                                                                                      TYPE: amino acid
                                                                                                                   TOPOLOGY:
                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                             h 15.2%;
Similarity 44.4%;
12; Conservative
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Pred. No. 2.00e+01
5; Mismatches
                                             Score 85; DB 3; Lo
Pred. No. 2.00e+01;
5; Mismatches 8
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RESULT 3

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AC XXXXXX

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CC Sequence 8, Appl1

CC Patent No. 56889

CC CONRESSE: CAL

CC ZIP: 91010

CC ASTORNATION FOI

CC TELEPHONE: CHACLE TYPE CHACLE

CC TYPE: MOLECULE TYPE CORGANISM: CC

CC TRAGMENT TYPE CC

ORGANISM: SOUENCE 1944 AM

CC SEQUENCE 1944 AM

CC ORGANISM: CORGANISM: 
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Best Local Similarity
Matches 18; Conser
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                                                                                                                                           Sequence 8, Application PC/TUS9305704
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                     Sequence 8, Application PC/TUS9305704
GENERAL INFORMATION:
APPLICANT: Edwards, Robert H
TITLE OF INVENTION: Vesicle Membr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Transposon 10
CORDACE 194 AA; 20868 NW; 201-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (818) 795-63: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                       1 MNSSTKIALVITLLDAM-GIGLIMPVLPTLLRE-FIASEDIANHFGVLLA-LYALMOV 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFIMARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION UNMBER: US/08/063,552
FILING DATE: 1993614
FILING DATE: 1993614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acid
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Farber, Michael B
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 756-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Edwards, Robert H
                                                                                                                                                                                                                                                                                                                                                                                               MGSGLPLVLLLTLLGSSHGTGPGMT-LQLKLKESFLTNSSYESSFLELLEKLCLLLHL 57
  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 225 So
CITY: Pasadena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.9%;
ilarity 31.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         795-6321
NO: 8:
                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vesicle Membrane Transport Proteins
Robert H
Vesicle Membrane Transport Proteins
17
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Pred. No. 2.75e+01;
13; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201442 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9067-1
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                                                                                                                                                                                                                                                                                                    194 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 194;
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APPLICATION NUMBER:

US/08/741,406

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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-741-406-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (818) 795-6321
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 anino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

NEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DAIA:
APPLICATION UNMER: PCT/US93/05704
FILING DATE: 19930611
CLASSIFICATION:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08741406 Patent No. 5721118
                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 14.9%;
Local Similarity 31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MNSSTKIALVITLLDAM-GIGLIMPVLPTLLRE-FIASEDIANHFGVLLA-LYALMQV 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGSGLPLVLLLTLLGSSHGTGPGMT-LQLKLKESFLTNSSYESSFLELLEKLCLLLHL 57
      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                              APPLICANT: Scheffler, Immo E.
TITLE OF INVENTION: Mammalian Artificial Chromosomes and
TITLE OF INVENTION: Methods of Using Same
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: PORT NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon &
                                                                                                                                                    STREET: 4370 La Jo
CITY: San Diego
STATE: California
                                                                                                                      COUNTRY: United States ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Transposon 10
ICE 194 AA; 20868 MW; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Farber, Michael B
REGISTRATION NUMBER: 32
                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
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California
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                                                                                                                                                                                         E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 South Lake Avenue, Ninth Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 83; DB 3; Length 194;
Pred. No. 2.75e+01;
13; Mismatches 23; Indels
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Best Local :
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                                                                     STATE: PA
STATE: PA
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSOQ for Windows Version 2.0
SOFTWARE: FASTSOQ TO WINDOWS Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,521
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
THING DATE: 19-MAR-1997
CLASSIFICATION BATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/550,717
PILING DATE: 31-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION UNMBER: 31.815
REFERENCE/DOCKET UNMBER: 9-UD 2317
TELECOMMUNICATION INFORMATION:
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-9091
INFORMATION FOR SED ID NO: 2:
FFORMATION FOR SED ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08820521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08820521 Patent No. 5942416
FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH50
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 SLPMAMSICHRGTGIALSAGVSL-FGMS-ALLLPGNFES-YLELVKSLCL 108
                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 14.7%;
Local Similarity 28.0%;
les 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                            APPLICANT: Fuetterer, Wendy
APPLICANT: Mao, Joyce
TITLE OF INVENTION: CDNA CLONE HNEDX20 THAT ENCODES
TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
JENCE 169 AA; 18610 MW; 162524 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 169 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                 Bergsma, Derk
Ganesh, Sathe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 82; DB 1;
Pred. No. 3.23e+01
20; Mismatches 1
                 GH50011
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Best Local :
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                                                                                             NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997.
REFERENCE_DOCKET NUMBER: FHOR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206), 622-8100
TELEFAX: (206), 224-0779
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332 YFSSSGFQADFHELLRRLCGL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/08252966B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
TELEX:
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 FLTNSSYESSFLELLEKLCLL 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match
Local Similarity 38.1%;
hes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                      ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFFMANDE: PC-DOS/MS-DOS
        TOPOLOGY: linear MOLECULE TYPE: protein DESCRIPTION: translation HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Eisenman, Robert N.
APPLICANT: Hurlin, Peter J.
APPLICANT: Ayer, Donald E.
TITLE OF INVENTION: Regulatory Proteins that Dimerize
TITLE OF INVENTION: Mad or Max
                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                            STREET: 1420 F:
CITY: Seattle
STATE: Washingt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 401 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                        LENGTH: 1253 amino ac
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 01-JUN-1994
                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 98101-2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ULE TYPE: protein
401 AA; 44386 MW; 855771 CN;
                                                                                                                                                                                                                                                                                                                              Washington
                                                                                   1253 amino acidS
                                                                                                                                                                                                                                                                                                                                                   E: Christensen, O'Connor, Johnson, and KindnessPLLC
1420 Fifth Ave., Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                           US/08/252,966B
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Pred. No. 3.78e+01;
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                                of.
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                                msina cDNA; see Figure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 401;
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Best Local
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                                           Matches
                                                     Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/08252966B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             949 VLGIKRDKSDSPAIQLRLKEPMDVDVEDYYPAFLDMVRSL 988
                     949 VLGIKRDKSDSPAIQLRLKEPMDVDVEDYYPAFLDMVRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Application US/08252966B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.5%;
Local similarity 27.5%;
hes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 LLGSSHGTGPGMTLQLKLKESF-LTNSSYESSFLELLEKL 51
                                                                                                                                                                                                                                            FILING DATE: 01-JUN-1994
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
REFERENCE/DOKET NUMBER: FIGOR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
 13 LLGSSHGTGPGMTLQLKLKESF-LTNSSYESSFLELLEKL
                                                                                                                                                                                                  TELEPHONE: (206) 682-8
TELEFAX: (206) 224-077
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                     MIDPOLOGY: linear MIDPOLOGY: linear MIDPOLOGY: protein DESCRIPTION: translation of msina9 cDNA; see Figure 29A, PROTEINAL: YES
                                                                                                                                                                                                                                                                                                                              APPLICANT: Elsenman, Rob
APPLICANT: Hurlin, Peter
APPLICANT: Aver Description
                                                                                      HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: MUS musculus
JENCE 1261 AA; 143711 MW; 7937040 CN;
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson, and KindnessPLLC STREET: 1420 Fifth Ave., Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ayer, Donald E.
TITLE OF INVENTION: Regulatory Proteins that Dimerize with
TITLE OF INVENTION. Mad or Max
NUMBER OF SEQUENCES: 19
                                                                                                                                                            LENGTH: 1261 amino
TYPE: amino acid
STRANDEDNESS: Sin
                                       14.58;
11 Similarity 27.58;
11; ConServa+***
                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1253 AA; 142589 MW; 7863283 CN;
                                                                                                                                                                                                                                                                                                                                                                                                    98101-2347
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                                                                                                                                                                                       1261 amino acids
                                                                                                                                                                 single
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                                                                                                                                                                                                                         224-0779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Robert N.
                                                                                                                                                                                                                                                                                                                          US/08/252,966B
                                                      Score 81; DB 1;
Pred. No. 3.78e+0
                                           14;
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                                             Mismatches
                                                                                                                                                                                                                                                          FHCR17694
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GENERAL INFORMATION:

STREET: 3174 POI CITY: Palo Alto

COUNTRY:

94304 Ç USA

US-08-828-832-4

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Sequence 6, Application US/07817920
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                                                                                                                                                                  60 GWSLPMAMSICHRGTGIALSAGVSL-FGLS-ALLVPGSFESH-LEFVKSLCL 108
                                                                                                                                                                                                        Y Match 14.3%;
Local Similarity 30.8%;
nes 16; Conservative
                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 169 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastsEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La1, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: NOVEL SUCCINATE DEHYDROGENASE SUBUNIT
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1705529
                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J
REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                            169 AA; 18389 MW; 161800 CN;
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                                                                                                                                                                                                                      Score 80; DB 2; 1
Pred. No. 4.43e+01.
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18; Mismatches
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TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 390 anino acids
                                                                 Sequence 6, Application US/08117006
           Sequence 6, Application US/08117006 Patent No. 5639652 GENERAL INFORMATION:
                                                                                                                                                                                                                              112 TDRWTLSQVVCD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/817,920
FILING DATE: 19920108
CLASSIFICATION: 514
ATTORNEY/ACENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/39318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/07817920
Patent NO. 5360735
GENERAL INFORMATION:
APPLICANT: Weinshank, Richard L
                                                                                                                                                                                                                                                                    66 HHARSQHHVVCN 77
                                                                                                                                                                                                                                                                                                           Match 14.3%;
Local Similarity 23.6%;
les 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
FRAGMENT TYPE: N-
IMMEDIATE SOURCE:
CLONE: 5-HT1DB
APPLICANT: Weinshank, Richard L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Branchek, Theresa
APPLICANT: Hartig, Paul R
TITLE OF INVENTION: DNA ENCODING
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 390 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
STATE: New York
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                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                           Score 80; DB 1; I
Pred. No. 4.43e+01;
22; Mismatches 32
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Best Local Similarity 23.6%;
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TELEX: 42253 COOP UI
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: amino acids
                                                                                                                                                                               PCT-US93-00149-6
                                                                    Sequence 6, Application PC/TUS9300149
GENERAL INFORMATION:
                                                                                                                                                                                                                                                   112 TDRWTLSQVVCD 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
                                                                                                                                                                                                                             66 HHARSQHHVVCN 77
                                                                                                                                                                                                                                                                           7 LVLLLTLLGSSHGTGPGMTLQLKLKESFL-TNSSYESSFLELLEKLCLLLHLPSGTSVTL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WOTGPEFFECT, VETSION 5.1
CURRENT APPLICATION DATA:
APPLICANT: Weinshank, Richard L.
APPLICANT: Harnchek, Theresa
APPLICANT: Hartig, Paul R.
TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HTLF RECEPTOR AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hartig, Paul R.
TITLE OF INVENTION: DAA ENCODING A HUMAN 5-HTIF RECEPTOR AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Branchek, Theresa APPLICANT: Hartig, Paul R.
                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE: N-IMMEDIATE SOURCE: 5-HT1DB
                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino a STRANDEDNESS: TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 30 Rockefeller Plaza CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/117,006 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
ZIP: 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                      390 AA; 43656 MW; 849817 CN;
                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
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Pred. No. 4.43e+01;
22; Mismatches 32;
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Best Local Similarity 23.6%;
Matches 17; Conservative
                                                Sequence 6, Application US/08216594
Patent No. 5652113
GENERAL INFORMATION:
APPLICANT: Weinshank, Richard L.
APPLICANT: Branchek, Theresa
APPLICANT: Hartig, Paul R,
TITLE OF INVENTION: DNA ENCODING A
TITLE OF INVENTION: AND USES THERE
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                              XXXXX
                                                                                                                                                                                                                  US-08-216-594-6
                                                                                                                                                  Sequence 6, Application US/08216594
                                                                                                                                                                                                                                                                                  112 TDRWTLSQVVCD 123
                                                                                                                                                                                                                                                            66 HHARSQHHVVCN 77
                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
                                                                                                                                                                                                                                                                                                       7 LVLLLTILGSSHGTGPGMTLQLKLKESFL-TNSSYESSFLELLEKLCLLLHLPSGTSVTL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00149
FILING DATE: 19930108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
CLONE: 5-HT1DB
                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
        NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STALL
COUNTRY: 10112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                CLONE: 5-HT1DB
NCE 390 AA; 43656 MW; 849817 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
New York
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                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                      DNA ENCODING A HUMAN 5-HT1F RECEPTOR AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                               Score 80; DB 3; L
Pred. No. 4.43e+01;
22; Mismatches 32
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STATE: N COUNTRY:

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TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 42253 COOP UI
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
                                                                                                                                                                                                                                                                      Sequence 6, Application US/08542358
                                                                                                                                                                                                            Sequence 6, Application US/08542358 Patent No. 5786155 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 TDRWTLSQVVCD 123
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                                                                                                                                                                                                                                                                                                                                                                                                                       66 HHARSQHHVVCN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Weinshank, Richard L.
APPLICANT: Branchek, Theresa
APPLICANT: Hartig, Paul R.
TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HTIE RECEPTOR AND USES THEREOF NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper 6 Dunham LLP
STREET: 1185 Avenue of the Americas
   COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: N-terminal
IMMEDIATE SOURCE:
CLONE: 5-HT1DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,
                                                                              STREET: 1185 A CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: unl
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               390 AA; 43656 MW; 849817 CN;
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ilarity 23.6%;
Conservative
                                                               New York
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Pred. No. 4.43e+01;
22; Mismatches 32
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                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                          398 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08370542
                                                                                                                                                                                                                                                                                                                                                                                                                                             XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-370-542-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08370542 Patent No. 5476782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 TDRWTLSQVVCD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 LVMLLALITLATTLSNAFVIATYYRTRKLHTPANYLIASLDVTDLLVSILVIPISTMYTV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 23.6%; les 17; Conservative
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 HHARSQHHVVCN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 LVLLLTLIGSSHGTGPGMTLQLKLKESFL-TNSSYESSFLELLEKLCLLLHLPSGTSVTL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 398 amino acids
                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                      APPLICANT: Weinshank, Richard L.
APPLICANY: Branchek, Theresa
APPLICANY: Hartig, Paul R.
TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HTIE RECEPTOR AND
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/39317-2Z/JPW/MAT
                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: N-terminal JENCE 398 AA; 44384 MW; 880684 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: un
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA
              APPLICATION NUMBER: FILING DATE:
                                                                                                                               COUNTRY: U.S.A. ZIP: 10112
                                                                                                                                                          CITY: New York
STATE: New York
                                                                                                                                                                                      ADDRESSEE: Cooper & Dunham STREET: 30 Rockefeller Plaza
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/542,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                         US/08/370,542
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Pred. No. 4.43e+01;
22; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     398 AA.
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۲, Gaps

STATE:

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Query Match Best Local S: Matches 1:

Local Similarity

SEQUENCE

RESULT

US-08-542-358-6

XXXXXX

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CC APPLICATION NUMBER: US/08/194,113
CC FILING DATE:
CC APPLICATION NUMBER: US/07/803.626
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC ATTORNEY/AGENT INFORMATION:
CC ATTORNEY/AGENT INFORMATION:
CC TELEPAX: 212-664-0525
CC TELEX: 422523 COOP UI
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 398 amino acids
CC TELEX: 422523 COOP UI
CC SEQUENCE CHARACTERISTICS:
CC MOLECULE TYPE: N-terminal
CC MOLECULE TYPE: N-terminal
CC MOLECULE TYPE: N-terminal
CC MATI-SENSE: NO
CC HAPOTHETICAL: NO
CC HAPOTHETICAL: NO
CC HAPOTHETICAL: NO
CC REAGNENT TYPE: N-terminal
SO SEQUENCE 398 AA: 44384 MM; 880684 CN;
OUETY MATCH
DE SEQUENCE 398 AA: 44384 MM; 806684 CN;
OUETY MATCH
SO SEQUENCE 398 AA: 44384 MM; 806684 CN;
OUETY MATCH
DE SEQUENCE CHARACTERISTICS I: Gaps 1:

OUETY MATCH
DE SEQUENCE CHARACTERISTICS II: Gaps 1:

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp Run on: protein - protein database search, using Smith-Waterman algorithm Fri Oct 22 18:42:40 1999; MasPar time 5.89 Seconds 530.469 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: Scoring table: PAM 150 Gap 11 >US-09-092-296-15 (1-78) from US09092296.pep 558 1 MGSGLPLVLLITLLGSSHGT......SGTSVTLHHARSQHHVVCNT 78

Searched: 122810 segs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries Database:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 39.113; Variance 85.189; scale 0.459

SUMMARIES

No. Score	L-3																16							
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Query Match	18.1	16.7	16.5	7	10.0	. C. T. S	15.9	15.8	15.6	15.6	15.4	15.2	•	15.1	•	•	•	٠		14.7	14.7	14.7	14.7	14.7
Query Match Length	501	382	712	л н Л -	202	879	3005	1822	143	396	272	315	441	454	509	378	401	469	647	56	110	110	152	155
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Description	protein export membra	Indianal cut- absent	Antico volument	cransiation regulator	osmotin-like protein	hypothetical protein	homeotic protein zfh-	K12H4.8 protein - Cae	5	probable translation		hypothetical protein	dihydroorotase (EC 3.	ne k	ical prote				Ō	mitotic-specific cycl	T-cell receptor alpha		antigen r	
Pred. No.	7 900-03		0.000	1.07e+00		•	2.46e+00				5.57e+00				9.51e+00	1.24e+01		1.24e+01	1.24e+01		1.61e+01			1 61 61 61

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772	742	741	402	387	331	191	141	132	1229	1219	482	474	469	387	346	346	787	107	3 6) u	2	
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A55004	A49672	148694	S23860	CBASN	D70431	H71370	G71079	A45159	A56068	I61713	B35843	T00943	H70626	A48326	JC5716	JC5715	S71192	8TC7CT	5/01/0	17000T		2#C⊢00
transcription factor	transcription factor	probable transcriptio	chloramphenicol resis		oligopeptide transpor	hypothetical protein	hypothetical protein	succinate dehydrogena	co-repressor protein	co-repressor protein	Lipopolysaccharide-bi	hypothetical protein	probable nark3 protei	ubiquino1cytochrome	G protein-coupled rec	G protein-coupled rec	mitosis-specific cycl	sperm acrosome antige	mota protein - Rhodob	ent-Kaurene synthase	THE PERSON PROCESS AND LAND	invasion profess inve
2.70e+01	2.70e+01				2.70e+01		2.70e+01	2.70e+01					2.09e+01				2.09e+01	2.09e+01	2.09e+01	1.61e+01		

ALIGNMENTS

RESULT 2 ENTRY TITLE ALTERNATE_NAMES ORGANISM DATE ACCESSIONS REFERENCE	Query Match Best Local Similarity Matches 18; Conser Matches 18; Conser Db 454 VILFOF-GSGPVKG Db 454 VILLTLLGSSHGTG	##IDJECTULE_TYPE DNA ##residues 1-55 . ##Cross-references 6 ##cross-references 7 ##cross-references 8 ##cross-references 8 ##cross-references 6 ##cross-references 6 #gene	#journal Natu	RESULT 1 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors
553538 #type complete ubiquinolcytochrome-c reductase (EC 1.10.2.2) cytochrome b - Allomyces macrogynus mitochondrion apocytochrome b #formal_name mitochondrion Allomyces macrogynus 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 08-Sep-1997 553538	Atch 18.1%; Score 101; DB 2; Length 501; 2al Similarity 38.3%; Pred. No. 7,90e-02; 18; Conservative 10; Mismatches 18; Indels 1; Gaps 1; VILFOF-GSGPVKGFATTLALGTIASFISNVYYAKVFLDLINSIKIL 499 1:1: : 1:	###COLUMN ###COLUMN ###COLUMN ###COS-references GB.AE000715; NID:g2983478; PID:g2983481; GB:AE000657 ##experimental_source strain VF5 CS ne	Nature (1998) 392:353-358 The complete genome of the hyperthermophilic bacterium Aquifex accilcus. Aquifex accilcus. ICO384 C70384 Cross Muldinary; nucleic acid sequence not shown; translation not shown	C70384 #type complete protein export membrane protein SecD - Aquifex aeolicus #formal_name Aquifex aeolicus 08-May-1998 #sequence_revision 08-May-1998 #text_change 12-Feb-1999 C70384 A70310 Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.; Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short, J.M.; Olson, G.J.; Swanson, R.V.

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KEYWORDS
FEATURE
10-340
10-210
222-340
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DATE
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REFERENCE
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#map_position 4R
KEYWORDS tra
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Best Local Similarity 33.3%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #introns
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#journal J. Mol. Biol. (1995) 255:688-701
#title The mitochondrial DNA of Allomyces macrogynus:
#cross-references MUID:96226032
                                                                                        #gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #accession
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                                                                                                                                                                                                                                                                                                                                                            #submission
                                                                                                                                                                                                                                                                                                                                                                                        #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #cross-references MUID:93180841
#accession A48156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues 1-382 ##label PAQ ##cross-references EMBL:U41288; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type DNA
                                                                                                                                                   ##experimental_source strain AB972
                                                                                                                                                                                                                                                         ##molecule_type DNA
##residues 1-712 ##label OLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##cross-references EMBL:Z68195; NID:g1122341; PID:e213795; PID:g1122344; NIPS:YDR211W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type DNA
                                                               ##cross-references SGD:S0002619; MIPS:YDR211w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 PVLSLANSFLIDSPLPSNITYLWNFGSLLG-LCLVIQIVTGVTLAMHYAPS 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A48156 #type cOmplete translation regulator GCD6 - yeast (Saccharomyces cerevisiae) guanine nucleotide exchange factor chain GCD6; protein YD8142B.03; protein YDR211w; translation initiation factor
                                                                                                                                                                                                                                                                                                                            S61576
Oliver, K.; Harris, D.
submitted to the EMBL Data
S61578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bushman, J.L.; Asuru, A.I.; Matts, R.L.; Hinnebusch, A.G. Mol. Cell. Biol. (1993) 13:1920-1932

Evidence that GCD6 and GCD7, translational regulators of GCNN, are subunits of the guanine nucleotide exchange factor for eIF-2 in Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A4815
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   translation regulation
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#domain cytochrome b6 homology #label CB6\
#domain pistoquinol-plastocyanin reductase 17K protein
homology #label 17K
gth 382 #molecular-weight 43467 #checksum 6973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      name Saccharomyces cerevisiae
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Pred. No. 8.03e-01
15; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                Library,
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                                                                                                                                                                                                                                                                                                                                                                December 1995
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#journal
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                                                                                                                                   *LILLE Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.

#Cross-references MUID:97105885

#accession $73757
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#cross-references MUID:97128324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##residues 1-252 ##label CHE
##cross-references GB:L76632; NID:g1220536; PID:g1220537
This protein is rich in cysteine content and play a part of the
##motecut-__ref
##residues 1-879 ##label HIW
##cross-references EMBL:AE000042; GB:U00089; NID:g1674112; PID:g1674117
##note the nucleotide sequence was submitted to the EMBL Data
Library, November 1996
                                                                                                                             ##status
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                                                                                     ##molecule_type DNA
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Similarity 39.5%;
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 16.3%;
Similarity 54.2%;
13; Conservative
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A flower-specific gene encoding
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osmottin-like protein precursor - tomato
smottin-like protein precursor - tomato
formal_name_tycopersicon esculentum #common_name tomato
13-Mar-1997 *sequence_revision 13-Mar-1997 *text_change
                                                                                                                                                                                                                                                                                                                                                                                              s/3/57 #type complete
hypothetical protein F11_orf879 - Mycoplasma
29342) (SGC3)
#format
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17-Jul-1998
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                                                                                                        preliminary; nucleic acid sequence translation not shown
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#product osmotin-like protein #status predicted #label
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Pred. No. 1.07e+00;
8; Mismatches 14
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                                                                                                                                                                                                                                                                     H.; Plagens,
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#authors
                                           CLASSIFICATION
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CLASSIFICATION #superfamily unassigned homeobox proteins; homeobox homology
KEYWORDS DNA binding; homeobox; nucleus; transcription regulation;
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DATE
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Best Local Similarity 38.0%;
19; Conservative
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2761-2817
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                                                                                                                  ##status preliminary
##molecule_type DNA
##residues 1-1822 ##label FAV
##cross-references EMBL:L14331; NID:g289702; PID:g289703
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##cross-references EMBL:M63450;
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##residues 1-30
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                  17/3; 72/1; 116/3; 170/1; 216/3; 340/3; 401/3; 444/3; 512/2; 634/3; 634/3; 745/1; 855/2; 1053/1; 1113/3; 1215/3; 1321/1; 1396/2; 1458/3; 1507/3; 1563/2; 1645/3; 1677/3; 1804/2 #superfamily unassigned DEAD/H box helicases; DEAD/H box helicase homology
                                                                                                                                                                                                                                                                                  Sequence of the S44849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fortini, M.E.; Lai, Z.; Rubin, G.M.
Mech. Dev. (1991) 34:113-122
The Drosophila zfr-1 and zfr-2 genes encode novel proteins containing both zinc-finger and homeodomain motifs.
                                                                                                                                                                                                                          Favello, A.D. submitted to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #length 3005
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20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
24-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S33642 *type complete homeotic protein zfh.2 - fruit fly (Drosophila melanogaster)
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llarity 28.9%;
Conservative
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Pred. No. 2.46e+00
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Pred. No. 2.46e+00;
15; Mismatches 11
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Query Match 15.6%;
Best Local Similarity 45.0%;
Matches 9; Conservative
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Best Local
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#title
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33-40
141-146
145-148
                                                                                                                                                                                                       #accession
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                                                                                                                               ##status preliminary
##molecule_type DNA
##residues 1-396 ##label GE
##cross-references EMBL:250142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-143 ##label THO
##cross-references EMBL:X73675, NID:9469952; PID:9469957
##note the nucleotide sequence was submitted to
Library, June 1993
#length 143 #molecular-weight 13317 #checksu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 15.6%;
Similarity 47.2%;
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 31.4%;
16; Conservative
                                                                                                                                                                                                                                                                                                 S58161 #type complete
probable translation releasing factor RF-1
(Schizosaccharomyces pombe)
SPAC2F7.17 protein
#formal_name Schizosaccharomyces pombe
13-Jan-1996 #sequence_revision 01-Mar-1996
                                                        57/3: 90/3
#superfamily translation releasing factor
#length 396 #molecular-weight 44954 #checksum
                                                                                                                                                                                                    submitted
S58161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thompson, J; Choudhury, S.; Kashanchi, F.; Doniger, J.; Berneman, Z; Frenkel, N.; Rosenthal, L.J. oncogene (1994) 9:1167-1175
A transforming fragment within the direct repeat region of human herpesvicus type 6 that transactivates HIV-1.
                                                                                                                                                                                                                                     Gentles, S.;
                                                                                                                                                                                                                                                     S58145
                                                                                                                                                                                                                                                                     S58161
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#region nucleotide-binding motif A (P-loop)\
#region nucleotide-binding motif B\
#region DEXH motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid sequence not shown;
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                                                                                                                                                                                                               5.; Churcher, C.M.
to the EMBL Data Library,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 87; DB 2; I
Pred. No. 4.25e+00;
4; Mismatches 14
Score 87; DB 2; I
Pred. No. 4.25e+00;
8; Mismatches
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Pred. No. 3.23e+00;
17; Mismatches 15
                                                                                                                         GEN
2; NID:g1052783; PID:91052800
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                                                ##experimental_source strain 168 GENETICS
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#gene
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                                                                                                                                                                                                                                                                                                                              #CrOss-references MUID:98044033
                                                                              ##molecule_type DNA
##residues_ 1-272 ##label KUN
##cross-references GB:Z99119; GB:AL009126;
#D:g2635457
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                                                                                                                                                                                                                                                                                                                                                                                                      Alloni, G.; Agasawara, N.; Moszer, I.; Albertini, A.M.;
Alloni, G.; Agavedo, V.; Bertero, M.G.; Bessieres, P.;
Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans,
A.; Braun, M.; Brighell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cumnings, N.J.;
Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;
Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandl, G.;
Guiseppi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood,
Guiseppi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood,
Guiseppi, G.; Krogh, S.; Kuenno, M.;
Kuetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.;
Kusahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi,
Y.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.;
Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno,
M.; Mosstl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly,
M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro,
V.; Pohl, T.M.; Portetelle, D.; Porwolik, S.; Prescott,
A.M.; Prescean, E.; Pujic, P.; Purnelle, B.; Rapoport, G.;
Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.;
Schloeter, R.; Scoffone, F.; Schiguchi, J.;
Schoete, B.; Rose, M.; Serror, P.; Shin, B.S.; Soldo,
B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.;
Terpstra, P.; Tognoni, A.; Tanakoshi, A.; Tanaka, T.;
Wanduutt, R.; Wedler, E.; Wedler, H.; Wantzenegger, T.;
Wanters, P.; Wedler, E.; Wedler, H.; Wantzenegger, T.;
Wanture (1997) 390:249-256
The commander of the Gram-rocation bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grundy, F.J.; Waters, D.A.; Takova, T.Y.; Henkin, T.M. Mol. Microbiol. (1993) 10:259-271
Identification of genes involved in utilization of acetate and acetoin in Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        $39641 #type complete
flagellar motor apparatus homolog ytxD - Bacillus subtilis
#formal_name Bacillus subtilis
08-Jun-1994 #sequence_revision 10-Nov-1995 #text_change
24-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S39641
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#superfamily flagellar motor rotation protein
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                                                                                                                                                  NID:g2635411; PID:e1185846;
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#authors Fleischmann, R.D., Adams, M.D.; White, O.; Clayton, R.A.;
Kirkness, E.F.; Kerlavage, A.R.; Bult. C.J.; Tomb, J.F.;
Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
Fitchugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;
Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
J.F.; Phillips, C.A.; Springs, T.; Hedblom, E.; Cotton,
M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek,
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann,
J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.;
Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.;
solence (1995) 269:496-512
#title Whole-genome random sequencing and assembly of Haemophilus
#cross-references MUID:95380630
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SUMMARY
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Best Local
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#title
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##molecule_type DNA
##molecule_type DNA
##residues 1-315 ##label TIGR
##cross-references GB:U32746; GB:L42023; NID:g1573626; PID:g1573627;
##cross-references GB:U32746; GB:L42023; NID:g1573626; PID:g1573627;
##cross-references GB:U32746; GB:L42023; NID:g1573626; PID:g1573627;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGSGLPLVLLLTLLGSSHGTGPGMTLQL--KLKESFLTNSSYESSFLELLEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.2%;
Similarity 29.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #superfamily conserved hypothetical protein HI00
#length 315 #molecular-weight 35906 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H04082 #type complete
hypothetical protein HI0830 - Haemophilus influenzae (strain
Rd KW20)
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                                                                     Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.;
Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Suglura, M.;
Sasamoto, S.; Kimura, T.; Hosouchi, T.; Muraki, A.; Nakazaki, N.; Narno, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
Yasuda, M.; Tabata, S.
                                                                                                                                                                                                                                                                                                                                                                          protein sll1018
                                                                                                                                                                                                                                                                                                                                                                                                                           S74800 #type complete dihydroorotase (EC 3.5.2.3) - Synechocystis sp. (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Н64082
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18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
DNA Res. (1996) 3:109-136
Sequence analysis of the genome of the unicellular
cyanobacterium Synechocystis sp. PCC6803. II. Sequence
                                                                                                                                                                                                                                                                                                                          #formal_name Synechocystis sp. PCC 6803
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                                                                                                                                                                                                                                                                                                    25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change
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Pred. No. 7.28e+
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Pred. No. 5.57e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
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                                                                                                                                                                                                                                                                       ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.1%;
Best Local Similarity 38.6%;
Matches 22; Conservative
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Best Local Similarity 32.7%;
Matches 16; Conservative
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#title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 GKPLALVPLNLSLRGNGVMREGPLAIQLGLPPDPVMSEAAVIASLLELL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues 1-454 ##label ENS | NID:g2337967; PID:g2337998 | ##cross-references EMBL:AF005370; NID:g2337967; PID:g2337998 | #checksum 4031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##cross-references EMBL:D90901; GB:AB001339; NID:g1651897; PID:g1652025
##note the nucleotide sequence was submitted to the EMBL Data
Library, June 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #Status
                                                                                                                                                                                                                                                                                                                                                                                                                 14
Naneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.;
Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.;
Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;
Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo,
S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
Yasuda, M.; Tabata, S.
DNA Res. (1996) 3:109-136
Sequence analysis of the genome of the unicellular
cyanobacterium Synechocystis sp. PCC6803. II. Sequence
determination of the entire genome and assignment of
potential protein-coding regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ensser, A., Pflanz, R.; Fleckenstein, B.
J. Virol. (1997) 71:6517-6525
Primary structure of the alcelaphine herpesvirus 1 genome.
T03130
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probable tyrosine kinase - alcelaphine herpesvirus 1
#formal_name alcelaphine herpesvirus 1
24 Mar-1999 #sequence_revision 24-Mar-1999 #text_change
                                                                                                                                                                                                                                                                         S76731
                                                                                                                                                                                                                                                                                                   25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change
                                                                                                                                                                                                                                                                                                                                             S76731 *type complete

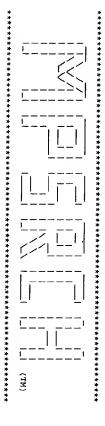
hypothetical protein - Synechocystis sp.

formal name Synechocystis sp.
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                                                                                                                                                                                                                                                                                        -Aug-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid sequence not shown; translation not shown
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Pred. No. 9.51e+00;
11; Mismatches 20
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Pred. No. 9.51e+00
16; Mismatches 1
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Search completed: Fri Oct 22 18:43:10 1999 Job time : 30 secs.
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                                                                                                                                              Query Match 14.9%; Score 83; DB 2;
Best Local Similarity 30.0%; Pred. No. 1.24e+
Matches 15; Conservative 18; Mismatches
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#title
                                                                                                                                                                                                                                                                                                                                                                                                       Aquifex aeolicus #cross-references MUID:98196666 #accession D70324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors
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                                                                                                                                                                                                                                                       #gene
                                                                                                      253 LPLGMLLGIFSASHAQALPESLRLHLDLILYGFGAFTIF-GGMLHLLPRI 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           402 GQGLPHYLLQDLLTEGEANQAEVNIQLTL-E-YLA 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##residues 1-509 ##label KAN
##cross-references EMBL:D90916; GB:AB001339; NID:g1653715; PID:d1019376;
##note the nucleotide sequence was submitted to the EMBL Data
Library, June 1996
                                                                                                                                                                                                                                                                                                           ##residues 1-378 ##label AQF
##cross-references GB:AE000681; N
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                                                                                                                                                                                                                                                                                        ##experimental_source strain VF5
                                                                                                                                                                                                                                                                                                                                               ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                         ##status
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Local Similarity 40.0%;
hes 14; Conservative
                                                                       5 LPLVLLLTLLGSSHGTG-P-GWTLQLKLKE-SFLTNSSYESSFLELLEKL 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GSGLPLVLLLTLLGSSHGTGPGMTLQLKLKESFLT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15
                                                                                                                                                                                                                                                                                                                                                                                                                                           Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.; Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short, J.M.; Olson, G.J.; Swanson, R.V.
Nature (1998) 392:353-358
The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
                                                                                                                                                                                                                              #length 378 #molecular-weight 43310 #checksum
                                                                                                                                                                                                                                                     aq_267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D70324 #type complete
hypothetical protein aq_267 - Aquifex aeolicus
#formal_name Aquifex aeolicus
08-May-1998 #sequence_revision 08-May-1998 #text_change
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translation not shown
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Pred. No. 9.51e+00;
7; Mismatches 12
                                                                                                                                                                                                                                                                                                         NID:g2982963; PID:g2982971; GB:AE000657
                                                                                                                                                                     DB 2; Length 378, 1.24e+01;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Fri Oct 22 18:43:27 1999; MasPar time 4.02 Seconds 548.762 Million cell updates/sec

Scoring table: Sequence: Description: Perfect Scor Score: РАМ 150 Gap 11 (1-78) from US09092296.pep 558 MGSGLPLVLLLTLLGSSHGT......SGTSVTLHHARSQHHVVCNT 78

>US-09-092-296-15

77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Swiss-prot37 1:swissprot

Statistics: Mean 40.060; Variance 77.694; scale 0.516

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	00	7	σ	ı UI	1.4	. ω	2	1	Result
80	80	80	81	81	81	81	81	81	82	82	83	83	83	83	84	85	86	87	88	89	91	92	Score
14.3	14.3	14.3	14.5	14.5	14.5	14.5	14.5	14.5	14.7	14.7	14.9	14.9	14.9	14.9	15.1	15.2	15.4	15.6	15.8	15.9	16.3	16.5	Query Match
387	191	169	482	387	346	346	261	253	385	372	1233	647	445	401	191	315	272	396	1822	3005	252	712	Query Match Length
1	Н	Н	1	Н	Ь	Н	Ь	Н	Н	j.,	۲	Н	Н	Н	_	\vdash	Н	۲	Н	ᆫ	Н	Н	BB
CYB_EMENI	Y064_TREPA	C560_BOVIN	LBP_RABIT	CYB_PODAN	GP42_HUMAN	GP41_HUMAN	ASPX_MOUSE	MOTA_RHOSH	CYB_ASPNG	INVE_SALTY	NME3_HUMAN	BGAL_MOUSE	YGCS_ECOLI	TCR2_ECOLI	YDB3_SCHPO	RSEB_HAEIN	YTXD_BACSU	RF1M_SCHPO	YM68_CAEEL	ZFH2_DROME	OLP1_LYCES	E2BE_YEAST	ID
CYTOCHROME B (EC 1.10.	HYPOTHETICAL PROTEIN T	SUCCINATE DEHYDROGENAS	LIPOPOLYSACCHARIDE-BIN	CYTOCHROME B (EC 1.10.	PUTATIVE G PROTEIN-COU	PUTATIVE G PROTEIN-COU	ACROSOMAL PROTEIN SP-1				GLUTAMATE [NMDA] RECEP	BETA-GALACTOSIDASE PRE		TETRACYCLINE RESISTANC	HYPOTHETICAL 21.1 KD P	SIGMA-E FACTOR REGULAT	HYPOTHETICAL 30.1 KD P	PUTATIVE MITOCHONDRIAL	HYPOTHETICAL HELICASE		OSMOTIN-LIKE PROTEIN P	TRANSLATION INITIATION	Description
1.15e+01	1.15e+01	1.15e+01	8.66e+00		8.66e+00	8.66e+00				6.52e+00		4.90e+00	4.90e+00		3.67e+00	2.74e+00	2.04e+00	1.52e+00	1.13e+00	8.33e-01	4.53e-01	3.33e-01	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31 .	30	29	28	27	26	25	24
77	77	77	78	78	78	78	78	79	79	79	79	79	79	79	79	80	80	80	80	80	80
13.8	13.8	13.8	14.0	14.0	14.0	14.0	14.0	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.3	14.3	14.3	14.3	14.3	14.3
1156	530	253	1239	991	490	267	101	1015	662	511	505	493	413	408	259	772	713	488	411	402	400
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HTS_DROME	UD18_RAT	POMA_VIBAL	NME3_MOUSE	BMP1_MOUSE	FA10_RABIT	YTXD_BACME	GRO_CRIGR	PTPX_HUMAN	GARP_HUMAN	MVIN_ECOLI	ACHB_BOVIN	ACHE_MOUSE	RF1M_YEAST	BTN1_YEAST	ATP6_YEAST	TF11_HUMAN	CDGT_BACSP	MBI1_EMENI	VGLM_HSVBC	OPDE_PSEAE	TCR8_PASMU
HU-LI TAI SHAO PROTEIN	UDP-GLUCURONOSYLTRANSF	CHEMOTAXIS POMA PROTEI	GLUTAMATE [NMDA] RECEP	BONE MORPHOGENETIC PRO	COAGULATION FACTOR X P	HYPOTHETICAL 29.3 KD P	GROWTH REGULATED PROTE	PROTEIN-TYROSINE PHOSP	GARP PROTEIN PRECURSOR	VIRULENCE FACTOR MVIN	ACETYLCHOLINE RECEPTOR	ACETYLCHOLINE RECEPTOR	MITOCHONDRIAL PEPTIDE	BIN1 PROTEIN.	ATP SYNTHASE A CHAIN P		_	MRNA MATURASE BI1 (COB	GLYCOPROTEIN M.	TRANSCRIPTION REGULATO	TETRACYCLINE RESISTANC
2.62e+01	2.62e+01	2.62e+01		2.00e+01		2.00e+01	2.00e+01	1.52e+01	1.52e+01	1.52e+01	1.52e+01	1.52e+01	1.52e+01	1.52e+01	1.52e+01	1.15e+01	1.15e+01	1.15e+01	1.15e+01	1.15e+01	1.15e+01

ALIGNMENTS

88888888888888888888888888888888888888	********	RESULT ID E AC P AC P DT 0 DT 0 DT 0 DT 0 DT 0 C C C C C C C C C C C C C C C C C C C
1 \$ 00 th	SEQUENCE FROM N.A. STRAIN-\$2386 / AB972; OLIVER K., SHORE L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.; OLIVER K., SHORE L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.; SUBMITTED (DEC-1995) TO EMBL/GENBANK/DDBJ DATA BANKS. -!- FUNCTION: SUBUNIT OF THE GUANINE NUCLEOTIDE EXCHANGE FACTOR FOR EIF-2. REQUIRED TO REPRESS GCN4 TRANSLATION UNDER NONSTARVATION CONDITIONS. GCD6 AND GCD7 REPRESS GCN4 EXPRESSION AT THE TRANSLATIONAL LEVEL BY ENSURING THAT RIBOSOMES WHICH HAVE TRANSLATION OF THE LEVEL BY ENSURING THAT RIBOSOMES WHICH HAVE TRANSLATED UORF1 WILL REINITIATE AT UORF2, -3, OR -4 AND THUS FAIL TO REACH THE GCN4 START SITE. -!- SUBUNIT: COMPLEX OF FIVE DIFFERENT SUBUNITS; ALPHA (GCN3), BETA (GCD7), GAMPA (GCD1), DELTA (GCD2) AND EPSILON (GCD6). -!- SIMILARLIY: BELONGS TO THE EIF-2B GAMMA/EPSILON SUBUNITS FAMILY.	EZBE_YEAST STANDARD; PRT; 712 AA. ### PRT
SEQUENCE FROM N.A. STRAIM-SABSC / AB972; OLIVER K., SHORE L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.; WALSH S.V.; SUBMITTED (DEC-1995) TO EMBL/GENBANK/DDBJ DATA BANKS. -!- FUNCTION: SUBUNIT OF THE GUANINE NUCLEOFIDE EXCHANGE FACTOR FOR THE FUNCTION UNDER NONSTARVATION CONDITIONS. GCD6 AND GCD7 REPRESS GCN4 EXPRESSION AT THE TRANSLATIONAL LEVEL BY ENSURING THAT RIBOSOMES WHICH HAVE TRANSLATED UCRE1 WILL REINITIATE AT UCRE2, -3, OR -4 AND THUS TO REACH THE GCN4 START SITE -!- SUBUNIT: COMPLEX OF FIVE DIFFERENT SUBUNITS; ALPHA (GCN3), BE (GCD7), GAMMA (GCD1), DELTA (GCD2) AND EPSILON SUBUNITS FAMIL -!- SIMILARITY: BELONGS TO THE EIF-2B GAMMA/EPSILON SUBUNITS FAMIL		LONGINE CHICAGO DUCCINICO DE DISTORIO DE LOS

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Best Local Similarity 54.2%;
Matches 13; Conservative
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OLPI_LYCES STANDAKU;

O41350;

O41350;

O1-NOV-1997 (REL. 35, CAST SEQUENCE UPDATE)

O1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

O1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

OSMOTIN-LIKE PROTEIN PRECURSOR.

LYCOPERSICON ESCULENTUM (TOMATO).

EUKARYOTA: VIRIDIPLANTAE: STREPTOHYTA: EMBRYOPHYTA; TRACHEOPHYTA;

EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLLOPHYTA; EUDICOTYLEDONS;

"""""TOTTAR: SOLANANAE; SOLANALES; SOLANACEAE; SOLANUM.
                                                                                                                     01-OCT-1994
01-OCT-1994
01-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 97128324.

CHEN R., WANG F., SMITH A.G.;

"A flower-specific gene encoding an osmotin-like protein from Lycopersicon esculentum.";

GENE 179:301-302(1996).

GENE 179:301-302(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z68195; E213795; -.
PIR; S30776; S30776.
PIR; A48156; A48156.
SGD; L0000674; GCD6.
PFAM; PF00132; hexapep; 3.
AMINO-ACID BIOSYNHHESIS; TRANSLATION REGULATION.
SEQUENCE 712 AA; 81161 MW; 5DAD189F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                           ZINC-FINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-CV. VF36;
    DROSOPHILA MELANOGASTER (FRUIT FLY)
                                                                                                                                                                                                                                       ZFH2_DROME
P28167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L76632; G1220537; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: CELL WALL PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CELL WALL; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00316; THAUMATIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 LPLSLETLLSLSQSTNPNFILTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 LGN-HGKNSDMDVEDRLQAVVLTDS-YETREMPLTAVKPRCLL
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252 AA;
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(REL. 30,
(REL. 30,
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llarity 39.5%;
Conservative
                                                                               PROTEIN 2 (ZINC-FINGER HOMEODOMAIN PROTEIN
                                                                                                                                                                                                                                                                             STANDARD;
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Pred. No. 3.33e-01
8; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 91; DB 1; L
Pred. No. 4.53e-01;
4; Mismatches 7
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                                                                                                                                                                                                                                                                             PRT;
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01-FEB-1994
01-NOV-1997
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28, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)

STANDARD;

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Query Match
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PIR; S33642; S33642.

FLYBASE; FEGN004607; zfh2.

PROSITE; PS00027; HOMEOBOX_1; 2

PROSITE; PS00028; ZINC_FINGER_C:

PROSITE; PS00071; HOMEOBOX_2; 3
                                                                                              DNA_BIND
DNA_BIND
ZN_FING
ZN_FING
DNA_BIND
SEQUENCE
             2165 QIKVLQEFFENNSYPKDSDLEYLSKL-LLLS-PRVIVVWFQNARQKQRKI 2212 |:|: : |: || | | | | | | | | | | :::| :: :
                                                                                                                                                                       REPEAT:
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE; 92001539.

FORTINI M.E., LAI Z., RUBIN G.M.;

FORTINI M.E., LAI Z., RUBIN G.M.;

"The Drosophila zfh-1 and zfh-2 genes encode novel proteins containing both zinc-finger and homeodomain motifs.";

MECH. DEV. 34:113-122(1991).

MECH. DEV. 34:113-122(1991).
                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00046; homeobox; 3.
PFAM; PF00096; zf-C2H2; 12.
HSSP; P15822; 4ZNF.
TRANSFAC; T00920; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA; METAZOA; ARTHROPODA; PTERYGOTA; DIPTERA; BRACHYCERA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M63450; G158823; -.
                                                                                                                                                                                                                                                                                                                                                                  TRANSFAC:
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                                                                                                                                                                                                                                                                                                                                                          zinC-finger; meTal-binding; dna-binding; homeobox; nuclear profein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NERVOUS SYSTEM.

- I SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).

- TISSUE SPECIFICITY: LARGELY RESTRICTED TO THE CNS OF LATE EMBRYO-

- SIMILARITY: CONTAINS THREE HOMEOBOX DOMAINS.
27
QLKLKESFLTNSSY-ESSFLELLEKLCLLLHLPSGTSVTLHHARSQHHVV 75
                                              Similarity
19; Conserv
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(larity 38.0%;
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                                                          Score 89; DB 1;
Pred. No. 8.33e-01
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C2H2-TYPE.
                                                                                                                                               HOMEOBOX 1. HOMEOBOX 2.
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_C2H2;
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                                                 Mismatches
                                                                                                8B4CC45F CRC32;
                                                                                                                                                                                                (DEGENERATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 94150718.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., WILSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A., BONTIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A., FRASTR A., FULTON L., BARDNER S., DU Z., DURBIN R., FAVELLO A., FRASER A., FUTON L., GARDNER A., GRREN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAM J., KIRSTEN J., LAISSTER N., LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SIMS M., SWALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSON R., WATERSON R., WATENSON R., WATENSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
                                                                                                                                                                                                                 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)
EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMY
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WORMPEP;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PFAM; PF00271; helicase_C; 1.
PFAM; PF00636; Ribonuclease_3; 2.
HYPOTHETICAL PROTEIN; HELICASE; ATP-BINDING; HYDROLASE; NUCLEASE; ENDONUCLEASE.
                 GENTLES S.,
                                                         SEQUENCE FROM N.A.
STRAIN-972;
                                                                                                                                                                                      SCHIZOSACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III K12H4.8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: WITH OTHER ATP DEPENDENT HELICASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "2.2 Mb of contiguous nucleotide sequence from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WOHLDMAN P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RHABDITINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 15.8%;
Local Similarity 31.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :| |:: ||| | :|::: ||:|: : :|| :: : :|| :: : : ||:
1 MGSGLPLVLLLTLLGSSHGTGPGMTLQ-L-KLKESFLTNSSYESSFLELLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K12H4.8; CE00273.
PS00517; RIBONUCLEASE_III; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33
145
1554
1822 AA;
                 CHURCHER C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RHABDITOIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELEGANS.
AZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
ABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40
148
1822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208291 MW; 4F8E56BE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                     PEPTIDE CHAIN RELEASE FACTOR PRECURSOR
                                                                                                                                                                                                                          SCHIZOSACCHAROMYCETACEAE;
             BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 88;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DECH BOX
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                                                                                                                                                                                                                                                                  ARCHIASCOMYCETES;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.13e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49
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PRESULT OF THE PROPERTY OF THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995
01-FEB-1995
15-DEC-1998
                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 98048467.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BACILLUS SUBTILIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RANSIT PEPTIDE.
    ,; Z99119;
S39641; S
    AF008220; G2293222;
Z99119; E1185846; -.
S39641; S39641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: BELONGS TO THE PROKARYOTIC AND MITOCHONDRIAL RELEASE FACTORS FAMILY. STRONG, TO YEAST MRF-1.
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z50142; G1052800; -. PROSITE; PS00745; RF_PROK_I;
                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL PROTEIN; PROTEIN BIOSYNTHESIS;
                                                281 LTHIPTGITVSMQDSRSQHQ
54 LLHLPSGTSVTLHHARSQHH 73
                                                                                                    Local Similarity 45.0%; les 9; Conservative
                                                                                                                                 15.6%;
45.0%;
                                                                                                                                                                                                                 44954 MW;
                                                   300
                                                                                                                                 Score 87; DB 1; L
Pred. No. 1.52e+00;
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                                                                                                                                                                                                                                        RELEASE
                                                                                                                                                                                                                                                               PUTATIVE MITOCHONDRIAL
                                                                                                                                                                                                                                                                                            MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                 988689CB CRC32;
                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                             MITOCHONDRION;
                                                                                                                                                        Length 396
                                                                                                       Indels
                                                                                                                                                                                                                                                               PEPTIDE CHAIN
                                                                                                    0;
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STANDARD; 31, CREATED)
31, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDATE KD PROTEIN IN ACUC 5'REGION BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE; PRT; 272 A (ORFA)

MEDLINE; 95020526.
GRUNDY F.J., WATERS D.A., TAKOVA TGRUNDY F.J., WATERS D.A., TAKOVA TIDENTIFICATION OF genes involved acetoin in Bacillus subtilis.";
MOL. MICROBIOL. 10:259-271(1993). TAKOVA T.Y., HENKIN T.M.; involved in utilization of acetate and

Q В

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EMBL outstation for

PROTEIN (POTENTIAL)

S.D.; Bacillus subtilis genes

SOFTTTT

WALSH S.V.;

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
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TRANSMEM
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01-NOY-1995 (REL. 32, CREATED)
01-NOY-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOY-1995 (REL. 32, LAST ANNOTATION UPDATE)
SIGMA-E FACTOR REGULATORY PROTEIN RSEB HOMOLOG PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.
KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.
MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
WITERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
FINE L.D., FRITCHMAN J.L., FUHRNANN J.L., GEOGHAGEN N.S.M.,
GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd."; SCIENCE 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSEB OR HI0630.
HAEMOPHILUS INFLUENZAE.
                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                          EMBL: U32746: G1573627; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-RD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACTERIA; PROTEOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSEB_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBCELLULAR LOCATION: PERIPLASMIC (POTENTIAL).
-1- SIMILARITY: TO E.COLI RSEB AND P.AERUGINOSA MUCB.
                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                 PERIPLASMIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 IGTLVGLVLMLKNLNDPHMLGPNMAIALLTTLYGSLLANMVFNPIAAKLEEK 215
                                                                                                                                                                                                                                                                                                                                                                                send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGSGLPLYLLLTLLGSSHGTGPGMTLQL--KLKESFLTNSSYESSFLELLEK
(BY SIMILARITY)
                                                                                                                                                                                                                                                                                                               HI0630;
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95350630.
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                                                                                                     Similarity
                                                                                                                                                                                                               ; -.
; SIGNAL.
1 23
315
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                                                                         15.2%;
larity 29.5%;
Conservative
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EIN; TRANSPORT; TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 P
58 P
174 P
208 P
272 P
30143 MW;
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                                                                                                                                                                                 35906 MW;
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POTENTIAL.
CYTOPLASMIC (POTEN
GESPECCCC32;
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                                                                            Score 85; DB 1; L
Pred. No. 2.74e+00;
18; Mismatches 11
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                                                                                                                                                                                                       POTENTIAL.
SIGMA-E FACTOR REGULATORY
HOMOLOG.
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                                                                                                                                                                                 80B1C11D CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLAYTON R.A., KIRKNESS E.F., DOUGHERTY B.A., MERRICK J.M.,
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                                                                               11;
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                                                                                                                             Length 315;
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  RAN MILER RAN MI
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P02980;
21-UUL-1986 (REL. 01, CREATED)
21-UUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-UUL-1986 (REL. 37, LAST ANNOTATION UPDATE)
TETRACYCLINE RESISTANCE PROTEIN, CLASS B (TETA(B)) (METAL-
TETRACYCLINE/H+ ANTIPORTER).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                           "Nucleotide:
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 84109550.
MEDLINE; 84109550.
MGUYEN T.T., POSTLE K., BERTRAND K.P.;
"Sequence homology between the tetracycline-resistance determinants of Tn10 and pBR322.";
GENE 25:83-92(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVLIN K., CHURCHER C. SUBMITTED (MAR-1996) 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; FUNGI; ASCOMYO SCHIZOSACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCR2_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                              MUIAGENESIS OF HIS-257. MEDLINE; 91177844.
                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 83143319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESCHERICHIA COLI
BACTERIA; PROTEO
                                                                                                          NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESCHERICHIA.
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-- SIMILARITY: BELONGS TO THE THIJ / PFPI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 15.1%;
Local Similarity 33.3%;
nes 14; Conservative
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                                                                                                          ACIDS
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                                                                                                                                                         SCHOLLMEIER K.;
e sequence of the Tn10 encoded
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     ADACHI K.,
                                                                                                          RES.
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                                                                                                          11:525-539(1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21078 MW; D47EB47B CRC32;
        AKASAKA T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAMMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 84; DB 1;
Pred. No. 3.67e+0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBDIVISION;
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1. Gaps

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Q46909;
01-NOV-1997 (
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SEQUENCE
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J. BIOL. CHEM. 265:15525-15530(1990).

J. BIOL. CHEM. 265:15525-15530(1990).

FUNCTION: RESISTANCE TO TETRACYCLINE BY AN ACTIVE TETRACYCLINE EFFLUX. THIS IS AN ENERGY-DEPENDENT PROCESS THAT DECREASES THE ACCUMULATION OF THE ANVIBLOTIC IN WHOLE CELLS. THIS PROTEIN FUNCTIONS AS A METAL-TETRACYCLINE/H-ANVIBORTER.

SUBCELULLAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.

SUBCELULLAR LOCATION: THE MAJOR FACILITATOR FAMILY (ALSO KNOWN AS THE DRUG RESISTANCE TRANSLOCASE FAMILY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruct use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; V00611; G43701; -. EMBL; J01830; G154847; -. PIR; A03507; YTECTO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (Stor send an email to license@isb-sib.ch).
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J., BIOL. CHEM. 266:6045-6051(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YAMAGUCHI A., ONO N., AKASAKA T., NOUMI T., SAWAI T.;
"Metal-tetracycline/H+ antiporter of Escherichia coli encoded by a
"ransposon, Tn10. The role of the conserved dipeptide, Ser65-Asp66,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUTAGENESIS OF 65-66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                MNSSTKIALVITLLDAM-GIGLIMPVLPTLLRE-FIASEDIANHFGVLLA-LYALMQV 55
                                                                                                                                                         MGSGLPLVLLLTLLGSSHGTGPGMT-LQLKLKESFLTNSSYESSFLELLEKLCLLLHL 57
                                                                                                                                                                                                                                                       Similarity
18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00216; SUGARIC RESISTANCE;
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ilarity 31.0%;
Conservative
(REL. 35, CREATED)
(REL. 35, LAST SEQUENCE UPDATE)
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257
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131
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214
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277
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                                                                       STANDARD:
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NOTE: TRANSMEMBRANE; INNER MEMBRANE; TRANSPORT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26
62
94
122
151
179
234
265
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                                                                                                                                                                                                                                                                                                                                             MW;
                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.

S-C: ALMOST NO CHANGE IN ACTIVITY.

S-A: NO CHANGE IN ACTIVITY.

D-N: UNABLE TO EXTRUDE TETRACYCLINE.

D-SE: MODERATE RESISTANCE TO

TETRACYCLINE.

H-SE: NO H+ TRANSLOCATION.

H-SE: NO H+ TRANSLOCATION.

G-> E (IN REF. 2).

V-> D (IN REF. 2).

V-> T (IN REF. 2).

Q-> E (IN REF. 2).
                                                                                                                                                                                                                                                    Pred.
13; 1
                                                                                                                                                                                                                                                                     Score 83; DB 1; I
Pred. No. 4.90e+00;
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                                                                                                                                                                                                                                                                                            Length 401;
                                                                                                                                                                                                                                                  Indels
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PRT; 647 AA.

V-1991 (REL. 20, CREATED)

O1-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

DE BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTA GALACTOSIDASE).

GN GLB1 OR GLB-1 OR BGL.

SMUS MUSCULUS (MOUSE).

C EUKARYOTA; METAZOA; CHOPT.

[1]

SPOOT
   Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                         Matches
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ECOGENE, EGL3116; YGCS.

PROSITE; PS00216; SUGAR_TRANSPORT_1; FALSE_NEG
PROSITE; PS00211; SUGAR_TRANSPORT_2; 1.

PFAM; PF00083; Sugar_tr; 1.

PFAM; PF00083; SUGAR_TRANSPORT; TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-KI2 / MG1655;

STRAIN-KI2 / MG1655;

MEDLINE; 97426617.

MEDLINE; 97426617.

MELATINER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V., RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHW G.F., GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U29579; G882664; ALT_INIT.
EMBL; AE000360; G1789130; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12."; SCIENCE 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GREGOR J., DAVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL METABOLITE TRANSPORT PROTEIN IN CYSJ-ENO INTERGENIC
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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ESCHERICHIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                    296 GALLGLVLTH-LLAHRKFLLGSFLLLAATLVVMACLPSGSSLTL 338
                                                                                                                                                                                                                                                                          23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE (POTENTIAL).
                                                                                                                                                                                                                                                                     GMTLQLKLKESFLTNSSYE-SSFLELLEKLCLLLHLPSGTSVTL
                                                                                                                                                                                                                                                                                                                                         Similarity
17; Conser
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274
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358
                               CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; THI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                        14.9%;
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                                                                                                                                                                                                                                                                                                                                    Score 83; DB 1; Pred. No. 4.90e+00 9; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                          CRC32;
                                                                                                                  (LACTASE)
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EMBL: M75122; G192185; J
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EMBL: M75100; G192185; J
EMBL: M75100; G192185; J
EMBL: M75101; G192185; J
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EMBL: M75112; G192185; J
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EMBL: M75115; G192185; J
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EMBL: M75118; G192185; J
EMBL: M75110; G192185; J
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"Organization of the mouse acid beta-galactosidase gene.";

"Organization of the mouse acid beta-galactosidase gene.";

"Organization of the mouse acid beta-galactosidase gene.";

"I SUBJECTION: CLEAVES BETA-LINKED TERMINAL GALACTOSYL RESIDUES FROM GANGLIOSIDES, GLYCOSPROTEINS, AND GLYCOSRMINOGLYCANS.

"I CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.

"I SUBJECTIVITY HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-GALACTOSIDES."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 91076843.

NANBA E., SUZUKI K.;

"Molecular cloning of mouse acid beta-galactosidase cDNA: sequence, expression of catalytic activity and comparison with the human enzyme.";

EIOCHEM. BIOPHYS. RES. COMMUN. 173:141-148(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entitles requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                         PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYDROLASE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: BELONGS TO FAMILY 35 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-BRAIN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MGI:88151; BGT
                              Similarity
       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS01182; GLYCOSYL_HYDROL_F35; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 301; Glycosyl_hydr17; GLYCOSIDASE; LYSOSOM
                                                                                            Conservative
                            14.9%;
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Score 83; DB 1; Louis Pred. No. 4.90e+00; 8; Mismatches 12;
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PROTON DONOR (POTEN
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                                                                                        W REF. 2).
W REF. 2).
B CRC32;
                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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O14957;
01-NOV-1997
                INVE_SALTY
P35671;
01-JUN-1994
01-FEB-1995
01-FEB-1996
INVASION PRO
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SUBMITTED (FEB-1996) TO EMBL/GENBARK/DOBJ DATA BANKS.

SUBMITTED (FEB-1996) TO EMBL/GENBARK/DOBJ DATA BANKS.

1. FUNCTION: NMDA RECEPTOR SUBTYPE OF GLUTAMATE-GATED ION CHANNELS POSSESSES HIGH CALCIUM PERMEABILITY AND VOLTAGE-DEPENDENT SENSITIVITY TO MAGNESIUM AND IS MEDIATED BY GLYCINE.

1. SUBUNIT: HETERODIMER OF AN EPSILON SUBUNIT AND A ZEIA SUBUNIT.

1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

1. SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
GLUTAMATE [NWDA] RECEPTOR SUBTUPE 2C) (NRZC) (NMDARZC).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIMATES; CATARRHINI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHANNEL;
                                                                                                                                                                                                                                                                                                                                           h 14.9%;
Similarity 33.3%;
20; Conservative
                     1994 (REL. 29,
1995 (REL. 31,
1996 (REL. 33,
N PROTEIN INVE.
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METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
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AL; TRANSMEMBRANE; POSTSYNAPTIC MEMBRANE; CALCIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAGNESIUM.
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                                                                                                                                                STANDARD;
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                                             , CREATED)
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                                                ANNOTATION
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2 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
4 (POTENTIAL).
FUNCTIONAL DETERMINANT OF NMDA RECEPTORS (BY SIMILARITY).
POTENTIAL.
POTENTIAL.
POTENTIAL.
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Pred.
13; N
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GLUTAMATE
EPSILON 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
W; 671F9981 CRC32;
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                                                                          UPDATE:
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4.90e+00;
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Query Match
Best Local Similarity '
Watches 12; Conserv
                                                                                                                                                                                                   CYB_ASPNG STANDARD: PRT; 385 AA. 233798; 15-DEC-1998 (REL. 37, CREATED) 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE) 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) CYTOCHROME B (EC 1.10.2.2). COB OR CYTB OR COBA. ASPERGILLUS NIGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M90714; -; NOT_ANNOTATED_CDS.
EMBL; U08280; G497226; -.
EMBL; X75302; E86775; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LODGE J.H., AMIN I.I., DOUCE G.R., BROWN N.L., STEPHEN J.;
SUBMITTED (SEP-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: INVOLVED IN THE TRIGGERING OF INTRACELLULAR EVENTS THAT LEAD TO MICROBIAL INTERNALIZATION OF THE INTESTINAL EPITHELIUM.
THESE EVENTS INCLUDE INCREASE IN CALCIUM LEVEL, REDISTRIBUTION OF ACTIN MICROFILAMENTS, AND CHANGES IN THE NORMAL STRUCTURE OF THE MICROVILLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRANIGA K., BOSSIO J.C., GALAN J.E.;
"The Salmonella typhimurium invassion genes invF and invG homologues of the AraC and PulD family of proteins.";
MOL. MICROBIOL. 13:555-568(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GINOCCHIO C., PACE J., GALAN J.E.;

'Identification and molecular characterization of a Salmonella typhimurium gene involved in triggering the internalization of salmonellae into cultured epithelial cells.";

PROC. NATL. ACAD. SCI. U.S.A. 89:5976-5980(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=SR11 / SL1344;
STRAIN=WU-2223L:
NARUSAWA T., KANAYAMA S., KIRIMURA K., USAMI S.;
"Nucleotide sequence of the apocytochrome b gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-TML;
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STRAIN=SR11 / SL
                                                                                   SEQUENCE FROM
                                                                                                                                                                                MITOCHONDRION
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SALMONELLA.
                                                                                                                                   EUROTIALES;
                                                                                                                                                              EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SALMONELLA TYPHIMURIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: TO YERSINIA OUTER MEMBRANE PROTEIN YOPN (LCRE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLC 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                           FUNGI; ASCOMYCOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372
                                                                                                                                TRICHOCOMACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                   N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SL1344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA; 42436 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A.
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                                                                                                                             A; EUASCOMYCETES; PLECTOMYCETES; MITOSPORIC TRICHOCOMACEAE; ASPERGILLUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 82; DB 1; I
Pred. No. 6.52e+00;
17; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A345002E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 372;
  of Aspergillus
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96
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385 AA;
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RESULT ID COLOR AND COLOR

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Query Match
Best Local Similarity
Matches 12; Conser
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EMBL; AB000575; D1035120; ...
EMBL; AB000576; D1035121; ...
EMBL; AB000577; D1035121; ...
EMBL; AB000578; D1035122; ...
EMBL; AB000583; D1035127; ...
EMBL; AB000583; D1035127; ...
EMBL; AB000583; D1035129; ...
EMBL; AB000597; D1035139; ...
EMBL; AB000597; D1035129; ...
EMBL; AB
                                                                                                                                                                                                                                                                                                                                                                   MOTA_RHOSH STANDARD; PRT; 253 AA. 053174; CFEMOTAXIS MOTA PROTEIN (MOTILITY PROTEIN A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                          RHODOBACTER SPHAEROIDES (RHODOPSEUDOMONAS BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WANG L., YOKOYAMA K., MIYAJI M., NISHIMURA K.; "The identification and phylogenetic relationship species of Aspergillus based on the mitochondrial MED. MYCOL. 36:153-164(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- COFACTOR: TWO HEME GROUPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: QH(2) + 2 FERRICYTOCHROME C
2 FERROCYTOCHROME C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               niger WU-2223L.";
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 ANISYLWNEGSLLA-LCLGIQIVTGVTLAMHYTPS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BOUND TO THE PROTEIN.
SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE:
CYTOCHROME C1 AND THE RIESKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUPLED TO ATP SYNTHESIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNSSYESSFLELLEKLCLLLHLPSGTSVTLHHARS
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SOCKETT R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conservative
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Pred. No. 6.52e+00;
11; MiSmatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IRON 1 (HEME B562 AXIAL LIGAND)
IRON 2 (HEME B566 AXIAL LIGAND)
IRON 2 (HEME B566 AXIAL LIGAND)
IRON 1 (HEME B566 AXIAL LIGAND)
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                                                                                                                                                                                                                                              SUBDIVISION; RHODOBACTER GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESPIRATORY CHAIN; TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AN ELECTROCHEMICAL POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IFM 41398, IFM 41399,
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                                                                                                                                                                                                                                                                                       SPHAEROIDES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WHICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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R EMBL; X85986; G758646; -.

JR PROSITE; PSO1307; MOTA; I TANSMENE; INNER MEMBRANE; WETTOTAXIS; FLAGELLA: TRANSMENE ION TRANSPORT.

FT TRANSMEN 2 49 POTENTIAL.

FT TRANSMEN 29 49 POTENTIAL.

FT TRANSMEN 146 166 POTENTIAL.

FT TRANSMEN 181 201 POTENTIAL.
Search completed: Fri Oct 22 18:43:49 1999 Job time : 22 secs.
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                                                                                                                                                                                                                                                                           Query Match 14.5%;
Best Local Similarity 27.5%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOL. MICROBIOL. 17:961-969(1995).

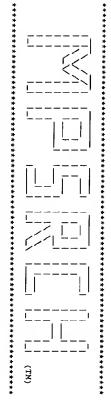
-!- FUNCTION: REQUIRED FOR ROTATION OF THE FLAGELLAR MOTOR. PROBABLE TRANSMEMBRANE PROTON CHANNEL (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.

-!- SIMILARITY: BELONGS TO THE MOTA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Analysis of the motA flagellar motor gene from Rhodobacter sphaeroides, a bacterium with a unidirectional, stop-start flagellum.";
                                                                                                                                 156 VGTLIGLYLMLGNMSDPKSIGPAMAVALLITLYGALMANVIF-APILNKLE 205
:|::|||:|:||:|:||
1 MGSGLPLYLLLTLLGSSHGTGPGMTLQL--KLKESFLTNSSYESSFLELLE 49
                                                                                                                                                                                                                                                                       Score 81; DB 1; Length 253; Pred. No. 8.66e+00; 20; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                           Gaps
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Oct 22 18:44:06 1999; MasPar time 8.07 Seconds
527.481 Million cell updates/sec

Tabular output not generated.

Title: >US-09-092-296-15

Description: (1-78) from US09092296.pep
Perfect Score: 558

Description: (1-78) from US09092296.pep
Perfect Score: 558
Sequence: 1 MGSGLPLVLLTLLGSSHGT......SGTSVTLHHARSOHHVVCNT 78
Scoring table: PAM 150
Gap 11

earched: 179066 segs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb19

sptrembly

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human

5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle

9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified

13:sp_vertebrate 14:sp_virus

Statistics: Mean 38.815; Variance 83.141; scale 0.467

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB B	ID	Description	Pred. No
1	101	18.1	501	2	067102	PROTEIN EXPORT MEMBRAN	8 2003
2	93	16.7	382	œ	Q37395	APOCYTOCHROME B (EC 1.	8.75e-01
w	92	16.5	209	N	068567	RESTRICTION ENDONUCLEA	1.17e+00
.4	92	16.5		14	P89688	ENV POLYPROTEIN.	1.17e+00
5	89	15.9		N	P75377	F11_ORF879 PROTEIN.	2 746+00
6	88	15.8	297	8	003305	CYTOCHROME B (FRAGMENT	3 63e+00
7	87		143	14	Q69582	HERPESVIRUS TYPE 6 DNA	4 79e+00
œ	86	15.4		4	Q14968	RHODOPSIN.	6.32e+00
وا	86	15.4	562	ű	Q23220	W08D2.3 PROTEIN.	6.32e+00
10	85	15.2		8	003294	CYTOCHROME B (FRAGMENT	8.31e+00
11	85			8	003295		8.31e+00
12	85	15.2		10	023674	CHALCONE SYNTHASE HOMO	8.31e+00
13	85	15.2	448	13	042453	SERPIN PRECURSOR.	8.31e+00
14	85	15.2	676	S	045649	K03D7.3.	8.31e+00
15	84	15.1	371	4	043190	PURINERGIC P2Y11 RECEP	1.09e+01
16	84	15.1	441	N	P72934	DIHYDROOROTASE.	1.09e+01
17	84	15.1	454	14	036385	PUTATIVE TYROSINE KINA	1.09e+01
18	84	15.1	509	N	P74537		1.096+01
19	84	15.1	1016	υ	017485		1 09e+01
20	84	15		1	017404		

45	44	43	42	41	40	ω 9	38	37	36	35	34	ω	32	31	30	29	28	27	26	25	24	23	2.2	22
82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	83	83	83	83	α	8 8
14.7	14.7	14.7	14.7	14.7	14.7	14.7	14.7	14.7	14.7	14.7	14.7	14.7	14.7	14.7	14.7	14.7	14.7	14.7	14.9	14.9		14.9		14.9
5825	1282	946	372	372	372	372	372	372	372	372	372	372	372	372	372	355	169	135	1236	711	385	378	297	244
10	11	ω	2	N	N	N	N	N	2	Ν	2	N	N	N	N	4	4	4	4	5	œ	N	œ	œ
082731	Q60520	013284	Q54026	Q54 030	Q54025	Q54028	Q54034	Q56052	Q54036	Q54037	Q54031	Q54029	Q57178	Q54032	Q54027	075774	Q99643	075609	015398	045825	063916	066624	003290	Q35487
	PAIRED AMPHIPATHIC HEL	м	_	INVASION PROTEIN.	_	INVASION PROTEIN.	INVASION PROTEIN.	INVASION PROTEIN.		INVASION PROTEIN.	INVASION PROTEIN.		INVASION PROTEIN.		INVASION PROTEIN.	771	INTEGRAL MEMBRANE PROT	INTEGRAL MEMBRANE PROT	N-METHYL-D-ASPARTATE R	T25E12.11 PROTEIN.	CYTOCHROME B.	HYPOTHETICAL 43.3 KD P	CYTOCHROME B (FRAGMENT	CYTOCHROME B (FRAGMENT
1.87e+01			1.87e+01	1.87e+01	1.87e+01	1.87e+01	1.87e+01	1.87e+01	1.87e+01	1.87e+01	1.87e+01	1.87e+01	1.87e+01	1.87e+01	1.87e+01			٠	1.43e+01	1.43e+01	1.43e+01	1.43e+01	1.43e+01	1.43e+0

ALIGNMENTS

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RESULT

ID

OF7102;
AC

O67102;
AC

O67102;
AC

O67102;
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O67102;
AC

O67102;
AC

OF70104WG-1998 (TREMBLREL. 0)
DT

O1-AUG-1998 (TREMBLREL. 0)
DT

O1-NOV-1998 (TREMBLREL. 0)
DE

PROTEIN EXPORT MEMBRANE PI
GN

SEQUENCE FROM N.A.

RESEQUENCE FROM N.A.

RA GRAHAM D.E., OVERBEEK R.,
RA FELDMAN R.A., SHORT J.M.,
RI

RI

RI

NATURE 392:353-358(1998).
RI

RR

SEQUENCE FROM N.A.

RC

STRAIN-VF5;
RA

GRAHAM D.E., OVERBEEK R.,
RA

FELDMAN R.A., SHORT J.M.,
RA

SEQUENCE 501 AA; 55459
RESULT . 2

ID 03735; PRELIMINARY; PRT; 382 AA.

AC 03735;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)

DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
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Best Local Similarity
Matches 18; Conser
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EMBL; AE000716; G2983481; -.

SEQUENCE 501 AA; 55459 MW; E67F690C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 98196666.

DECKET G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACTERIA; AQUIFICALES; AQUIFICACEAE; AQUIFEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NATURE 392:353-358(1998).
                                                                                                                                                                                                                                                    454 VILEQE-GSGPVKGFATTLALGTIASFISNVYYAKVFLDLLNSLKIL 499
                                                                                                                                                                                                               8 VLLLTILGSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLCLL 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                 18.1%; Score 101; DB 2; Length 501; 38.3%; Pred. No. 8.20e-02; vative 10; Mismatches 18; Indels
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07, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
PROTEIN SECD.
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Best Local :
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068567;
068567;
01-AUG-1998
01-AUG-1998
01-AUG-1998
TLI 4
P89688
P89688;
01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BADRII;
ZHANG B.-H., WILSON G.G.;
SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF051092; G2995645; -.
ENDONUCLEASE.
ENDONUCLEASE.
SEQUENCE 209 AA; 23834 MW; 1EC63D0B CRC32;
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BLASTOCLADIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAQUIN B., LAFOREST M.J., LANG B.F.;
SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-:- CATALYTIC ACTIVITY: QH(2) + 2 FERRICYTOCHROME C =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDILINE; 96226322.

PAQUIN B., LANG B.F.;

PAQUIN B., LANG B.F.;

"The mitochondrial DNA of Allomyces macrogynus: the complete genomic sequence from an ancestral fungus.";

J., MOL. BIOL. 255:688-701(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
APOCYTOCHROME B (EC 1.10.2.2) (UBIQUINOL--CYTOCHROME C REDUCTASE)
(CYTOCHROME BC1 COMPLEX).
COB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U41288; G1236404; --
PFAM; PF00032; Cytochrome_b_C; 1.
PFAM; PF00033; Cytochrome_b_N; 1.
OXIDOREDUCTASE; MITOCHONDEION.
SEQUENCE 382 AA; 43467 MW; A21E1AB1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALLOMYCES MACROGYNUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                      88
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                                                                                                                                                                                                                                                                                                                                                                                                                             GDDVSHYLIYRVLGVAQEEGRLIDVYQN-KGRFLYK--YAGSFLEAATKLCFKEAFPDSA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGMTLQLK-LKESFL-TNSSYESSFLELLEKLCLLHLPSGTSVTLHHARS
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                                                                                                                                                                                                                    SYTLHHARSQH 72
                                                                                                                                                                                                                                                                                      SLRLPNTQGQR 98
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20; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEOBACTERIA; GAMMA SUBDIVISION; LYSOBACTERALES; AS GROUP; XANTHOMONAS.
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8 (TREMBLREL. 07, LAST)
8 (TREMBLREL. 07, LAST)
N ENDONUCLEASE R.XBAI.
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ilarity 33.3%;
Conservative
   (TREMBLREL. 03,
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larity 28.2%;
Conservative
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                                                                         PRELIMINARY;
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ALLOMYCES.
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07, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
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Pred. No.
21; Misma
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Pred. No.
   CREATED;
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                                                                         863
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1.17e+00;
atches 27; Inde1s
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8.75e-01;
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Best Local S
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01-FEB-1997 (TREMBLREL. 08, LA
01-NOY-1998 (TREMBLREL. 08, LA
FIL_ORF879 PROTEIN.
MYCOPLASMA PREUMONIAE.
BACTERIA; FIRNICUTES; BACILLUS
MYCOPLASMATACEAE; MYCOPLASMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 5
P7S377
P7S377;
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"Proviral organization and sequence analysis of feline
immunodeficiency virus isolated from a Pallas' cat.";
VIROLOGY 228.84-91(1997).
EMBL; US6928; G1899040; -.
POLYPROTEIN.
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MEDLINE; 9601385S.
BARR M.C., ZOU L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1997 (TREMBLREL. 01-NOV-1998 (TREMBLREL.
                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-M.129;
HIMMELREICH R., HILBERT H., LI B.-C.;
SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; AB000042; G1674117; -.
SEQUENCE 879 AA; 101086 MW; 94D217E0 CRC32;
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                                                                                                                                                                                                                                                                                                                                                               "Complete sequence analysis of the genome pneumoniae.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 97105885
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MEDLINE; 97177285.
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VIRUSES; RETROID VIRUSES; RETROVIRIDAE; LENTIVIRUS
                            677
                                                                                                                                                                                                                                                                                                                                                                                                                HERRMANN R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                          NUCLEIC ACIDS RES.
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EGIPKDSNY-SSFVHLLDQKSLFLQLAKVSGIDINENK 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
23; Conser
                                                                        h 18.9%;
Similarity 28.9%;
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   863 AA;
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ilarity 33.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACILLUS/CLOSTRIDIUM GROUP; MOLLICUTES,
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08, LAST ANNOTATION UPDATE)
                                                                        Score 89; DB 2;
Pred. No. 2.74e+(
15; Mismatches
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Pred. No. 1.17e+00;
16; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                       PLAGENS H.,
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LAST ANNOTATION UPDATE)
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Best Local
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Q69582;
Q1-NOV-1996 (TREMBLREL. 0
Q1-NOV-1996 (TREMBLREL. 0
Q1-NOV-1998 (TREMBLREL. 0
Q1-NOV-1998 (TREMBLREL. 0
Q1-NOV-1998 (TREMBLREL. 0
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01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE
CYTOCHROME B (FRAGMENT).
CARETTOCHELYS INSCULPTA (PITTED-SHELLED TURTLE).
                                                                                                                                                                                                                                                                                                                                          "A transforming fragment within the direct repeat region of human herpesvirus type 6 that transactivates HTV-1.", ONCOGENE 9:1167-1175(1994).
EMBL: X73675; G469957:
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MEDLINE; 94181269.
THOMESON J., CHOUDHURY S., KASHANCHI F., DONIGER J., BERNEMAN 2.,
FRENKEL N., ROSENTHAL L.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
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SHAFFER H.B., MEYLAN P., MCKNIGHT |
SYST. BIOL. 0:0-0(0).
-!- CATALYTIC ACTIVITY: QH(2) + 2
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN HERPESVIRUS-6
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                                                                                    88
                                                                                                                                                                                                 Local
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        Similarity
17; Conser
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Similarity 31.5%;
17; Conservative
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297 AA;
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33587 MW;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                    Score 87; DB 14;
Pred. No. 4.79e+00;
4; Mismatches 14
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LAST SEQUENCE UPDATE)
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Pred. No. 3.63e+00
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                                                                                                                                                                                                                                                                                                         597857A6 CRC32;
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                                                                                                                                                                                                                             Length 143;
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MEDLINE: 94150718.

MILSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A., BONDIELD J., BERTON J., CONNELL M., COPSEY T., COOPER J., COULSON A., EDRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., CHANGER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KITSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPER A., SUNDERS D., SHOWNKEEN R., STALDON N., SMITH A., SOUNHAMMER B., STALDON R., SULTON J., THEERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

"2.2 Mb of contiguous nucleotide sequence from chromosome III of C."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q23220 PRELIMINARY, Q23220; Q232200; Q232200; Q232200; Q232200; Q232200; Q23220; Q23220; Q23220; Q232200; Q232200; Q232200; Q232200; Q
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Q14968; O1-NOV-1996 (TREMBLREL. 0
01-NOV-1996 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
                                                                                                                                                                                                                                                                        "2.2 Mb of contiguous nucleotide elegans."; RNATURE 368:32-38(1994). EMBL; Z70Z71; E1350111; -.
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CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA;
RHABDITINA; RHABDITOIDEA; RHAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KUNZ D., GERARD N.P., GERARD C.;
"The human leukocyte platelet-activating factor receptor. cDNA cloning, cell surface expression, and construction of a novel epitope-bearing analog.",
J. BIOL. CHEM. 267:9101-9106(1992).
EMBL, M76676; G189270; -.
EPAM; PF000001; 7tm_1; 2.
                                                                                                                                                                                                                                            SEQUENCE
                               SEQUENCE FROM N.A. MEDLINE; 94150718.
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EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RHODOPSIN
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                                                                                                                                                                                  Match
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   LVLLLTLLGSSHGTGPGMTLOLKLKESFLTNSSYESSFLELLEKLCLLLHLPSGTSVTLH
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                                                                                                                                                                                                                                     Z70271; E1350
NCE 562 AA;
                                                                                                                         Similarity
23; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322 AA;
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ilarity 31.5%;
Conservative
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.R-1996) TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 86; DB 4; Len
Pred. No. 6.32e+00;
V4smatches 22;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                  Score 86; DB 5; Le
Pred. No. 6.32e+00;
19; Mismatches 27;
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                                                                                                                                                                                                                                     5272E400 CRC32;
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SECUENCE
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TRACHEMYS SCRIPTA (RED-EARED SLIDER TURTLE).
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SHAFFER H.B., MEYLAN P., MCKNIGHT M.L.;
SYST. BIOL. 0:0-0(0).
-i- CATALYTIC ACTIVITY: QH(2) + 2 FERRI
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SYST. BIOL. 0:0-0(0).
-!- CATALYTIC ACTIVITY: QH(2) + 2 FERRICYTOCHROME C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1997 (TREMBLREL 04, 01-JUL-1997 (TREMBLREL 04, 01-NOV-1998 (TREMBLREL 08, CYTOCHROME B (FRAGMENT).
                                                                                                                             PROSITE: PS00192; CYTOCHROME_B_HEME; 1. PFAM; PF00033; CYTOCHIOME_D_C; 1. PFAM; PF00033; CYTOCHIOME_D_N: 1. MITOCHONDRION; ELECTRON TRANSPORT; RESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00032; cytochrome_b_C: 1.
PFAM; PF00033; cytochrome_b_N; 1.
MITOCHONDRION; ELECTRON TRANSPORT; RESPIRATORY CHAIN; TRANSMEMBRANE;
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EUKARYOTA; MET
                                                                                                        HEME.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                               FERROCYTOCHROME C.
COFACTOR: TWO HEME GROUPS
(B562 AND B566) WHICH ARE NOT COVALENTLY
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COFACTOR: TWO HEME GROUPS
(B562 AND B566) WHICH ARE NOT COVALENTLY
(BY SIMILARITY)
                                                                                                                                                                                                                                                                                                   (BY
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re; PS00192; CYTOCHROME_B_HEME; 1.
                                                                                                                                                                                                                                                                 U81351; G2098693; -
                                                                                                                                                                                                                                                                                                SIMILARITY)
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DEA; BATAGURIDAE; HEOSEMYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METAZOA; CHORDATA; VERTEBRATA;
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ilarity 32.1%;
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          AA;
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Pred. No. 8.31e+00;
11; Mismatches 25;
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                                                                                                                                RESPIRATORY CHAIN; TRANSMEMBRANE;
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Best Local Similarity 33.3%;
Matches 18; Conservative
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042453;
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SEQUENCE FROM N.A., CONWAY A.R., DAVIS K., BRENDEL V., FEDERSPIEL N.A., CONWAY A.R., CONWAY A.R., DAVIS K., BRENDEL V., PALM C.J., AU M., ARAUJO R., CHUNG E., KURIZ D.B., BUEHLER E., DEWAR K., FENG J., KIM C., LI Y., SHINN P., SUN H., OJI O., DEWAR K., SHEN Y.K., TORIUMI M., VYOTSKAIA V., YU G., THEOLOGI: BCKER J., DAVIS R. W.;

SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

EMBL; U89959; G2317904; -.

EMBL; U89959; Chal_stil_synt; 1.

FPAM; PF00195; Chal_stil_synt; 1.

FPAM; PF00195; Chal_stil_synt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 023674
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                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-LARVAL LIVER:
TISSUE-LARVAL LIVER:
ROBSON P., YOUSON J.H., KEELEY F.W.;
SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AP009964; G2275601; -.
PFRAM: PF00079; SETPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SERPIN PRECURSOR.

PETROMYZON MARINUS (SEA LAMPREY).

EUKARYOTA; METAKOA; CHORDATA; VERTEBRATA; CEPHALASPIDOMORPHI;

PETROMYZONTIFORMES; PETROMYZONTIDAE; PETROMYZON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA, VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MANNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 GLTLVHLLFLHETGSNNPTGLNSNVD-KIPFHPYFSYKD-LLGIILMLTLLLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 TLLALGKAFPSQVVPQENLVEGFLRDTKCDDAFIKEKLEHLC 68
                                         82 LMMLLAGSGDKTETQLTNALRL-Q-FLRDPNPQASFQALVSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
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LLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKL
                                                                                                                                  h 15.2%;
Similarity 34.9%;
15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 15.2%;
Similarity 33.3%;
14; Conservative
                                                                                                                                                                                                                                                                         22
448 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                              21
448
                                                                                                                                                                                                                                                                         21 POTENTIAL.
448 SERPIN.
49044 MW; 6E233618 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08,
05,
05,
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Pred. No. 8.31e+00;
12; Mismatches 15
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Pred.
9; M
                                                                                                                               Score 85; DB 13;
Pred. No. 8.31e+00;
12; Mismatches 14
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LAST SEQUENCE UPDATE)
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J. 8.31e+00;
Thes 25;
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                                                                                                                                                                                                             Length 448;
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                                                                      122
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RA BONFIELD J., BURTON J., CONNELL M., COPER J., COULSON A.,
RA BONFIELD J., BURTON J., CONNELL M., COPER J., COULSON A.,
RA GRANTON M., DEAR S., DU Z., DUBEIN R., FAVELLO A., FULTON L.,
RA GRADNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGIAN M.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGIAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA THIERRY-MIEG J., THOMAS K., VADUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WELLNSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
RA WATSON A., WELNSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
RA WATSON A., WELNSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
RA WATSON A., WELNSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
RI "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RI "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RI "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RI "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RI "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RI "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
REMBL: Z81562; E1188135; -.
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Best Local (
                                                                                                                                                                Matches
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O45649 PRELIMINARY;
O15649;
O1-JUN-1998 (TREMBLREL 06, C
O1-JUN-1998 (TREMBLREL 08, L
O1-NOV-1998 (TREMBLREL 08, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O43190 PRELIMINARY; PRT; 371 AA.

O1-JUN-1998 (TREMBLEEL 06, CREATED)

O1-JUN-1998 (TREMBLEEL 06, LAST SEQUENCE UPDATE)

O1-JUN-1998 (TREMBLEEL 06, LAST ANNOTATION UPDATE)

PURLINERGIC P2Y11 RECEPTOR.
                                                                                                                                                                                                                                                                                               COMMUNI D., GOVAERTS C., PARMENTIER M., BOEYNREMS J.M.;
J. BIOL. CHEM. 0.0-0(1997).
EMBL; AF030335; G2574120; -.
SEQUENCE 371 AA; 40174 MW; 5686F41C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-PLACENTA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MATTHEMS L.;
SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K03D7.3.
CAENORHABDITIS ELEGANS.
CUKARYOTA; METAZOA; NEWATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE: 94150718.
                                             y Match 15.1%; Score 84; DB 4; Length 371;
Local Similarity 38.1%; Pred. No. 1.09e+01;
hes 16; Conservative 12; Mismatches 11; Indels
1 MGSGLPLVLLLTLLGS-SHGT--GPGMTLQLKLKESFLTNSS 39
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Search completed: Fri Oct 22 18:44:57 1999 Job time : 51 secs.

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fomo sapiens sequence 1 f	Sequence 22 fustela viso	domo sapiens domo sapiens sequence 5 f	domo sapiens Sequence 22	Homo sapiens Sequence 14	Descriptio	predicted by che score of the restoral score dist	2; scale 1.99	11 20:gb 25:gb_pa1 23:gb_un 36:gb_un	un 4:em_htg 10:em_ov 11: sts 16:em_vi		ses x 2				MasPar time 456 1390.417 Millio	using Smith-Wat	ng din 1ec	
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2.76e-01 2.76e-01 9.88e-01	. 48e-	1.30e-03 1.30e-03	400	69e-	ed.	e a printed,		in1 7:9b_p11	em_hum2 Lph					NGGGACCA 229	onds updates/sec	orithm		**************************************
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									130 23 25
ALIGNMENTS	PFAPA2B AB010141S4 HS508I15 AP000031	AC003059 I41364 I41363	HS460JB AC005772 AC005920 AC005096	AC006252 HS593C16 AC005558 AC006060	AC006542 AP000029	HSA010901 NMSERBORF D63997	DROSYT MMBAKEXN E10775 AR014574	D87227 HS156G5R HUMGOLGINB	MVU87256 HUMPFUCAS AC003999 AC004947 A62994
	um knowles llus gene sequence	Mouse Chromosome 10 BA Sequence 144 from pate Sequence 143 from pate	n DNA sequence * sapiens chromos sapiens chromos	sapiens 3p21.1 c n DNA sequence ** ophila melanogast sapiens 3p22-8 p	ING DRAFT SEQU	Homo sapiens MUC4 gene Neisseria meningitidis Homo sapiens mRNA for	D.melanogaster synapto Mus musculus Bak gene, DNA encoding part of A Sequence 1 from patent	oma lon	Mustela vison GT dinuc H.sapiens fucosidase p Human PAC clone DJ1139 Homo sapiens clone DJ1 Sequence 6 from Patent
	3.79e+01 3.79e+01 3.79e+01 3.79e+01 3.79e+01	1.16e+01 1.16e+01 3.79e+01 3.79e+01							9.88e-01 3.44e+00 3.44e+00 3.44e+00 1.16e+01

REFERENCE AUTHORS TITLE REFERENCE AUTHORS VERSION KEYWORDS SOURCE ORGANISM RESULT 1 LOCUS DEFINITION ACCESSION NID COMMENT TITLE JOURNAL REMARK REMARK JOURNAL LISM Homos sapiens Bukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Gatarrhini; Hominidae; Homo. CL (bases 1 to 47323) RS Janer,M., Guillaudeux,T., Vu.O., Kutyavin,T., Harter,H. and Geraghty,D.E. Large scale sequence analysis of the human MHC class I region MI Unpublished (1998) K Fred Hutchinson Cancer Research Center The Clinical Research Division The Clinical Research Division 100 Fairview Ave. N., P.O. Box 19024 Seattle, WA 98195-1024 Seattle, WA 98195-1024 Seattle, WA 98105, USA Winversity of Washington, Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA University of Washington Human Genome Center Box 352145 Seattle, WA 98195 Contact: Daniel E. Geraghty (geraghty@fhorc.org) 5: UWGC: 970m23.013 (Genbank Accession: AC005530) 3/: UWGC: 970m23.013 (Genbank Accession: AC004211) Sequence Quality Assessment: This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than AC005937 47323 bp DNA PRI 05-NOV-1998 HOMO Sapiens clone UWGC:370M23.002 from 6p21, complete sequence. AC005937 g3845393 AC005937.1 GI:3845393 HTG.

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FEATURES
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This sequence has been validated by Multiple Complete Digest
This sequence has been validated by Multiple Complete Digest
Mapping. Comparison of the experimentally derived map digest
fragments with sequence-predicted fragments is given below.
Small fragments below a variable cutoff (approximately 400-600bp)
Small fragments below a variable cutoff (approximately There are no
are not mapped and hence do not appear in the table. There are no
significant remaining discrepancies between the experimental and
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Base-by-base quality values are not generally visible from the Genhank flat file format but are available as part of this entry's ASN.1 file.
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/rpt_family="Alu"
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/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                           complement(21287
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                                                                                                                                                                                                                                                                                                                                                               clone_lib="Research Genetics BAC Library"
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                  BASE COUNT
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                                                                                                                                                                                                                                         ACCESSION
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Best Local Similarity 100.0%;
Matches 108; Conservative
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166494.1
                                                                                                                                                                                                                                      7218 bp
Sequence 14 from patent
156494
                                          l (bases 1 to 7218)

l (bases 1 to 7218)

Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.

Recombinant fowlpox virus

Patent: US 5670367-A 14 23-SEP-1997;

Location/Qualifiers

1. .7218
                                                                                                                                                              Unknown
                                                                                                                                                                              Unknown.
                                                                                                                                             Unclassified.
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/rpt_fam11y-"MIR"
37372. .37648
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                  /organism="unknown"
1491 c 1486 g
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US 5670367.
                       1929
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                       368
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Length 7218;

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Query Match 14.4%;
Best Local Similarity 14.6%;
Matches 26; Conservative
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Best Local Similarity
Matches 5; Conse
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                                                                                                                                                                                                                                                                                                                                                                                                              126 TGCAAAGTCATACCCCGGCCCTGTTCCATGTGAGCTGCCAAGGAGGGTCAAGAGGAGGACA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 ATTCCAGGAAGCTGGACTCATAGGAGGAATTTGTCAGAAAAGACTCCTTCAGCTTC-AGT 127
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                                                                                                                                                                                                                                                                                                                              66 AGGGGCAGCCCCATAGTGGCCACTGCGCTCCTGGGATGGAGGAAAACTGAA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YSSANYNYGGNNVGAAKTHYYTHTNVSGADSKTVTDSYNASGTSSSNGGTD-GNRSGADS 119
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g3337381
AC004787.1
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Plant inhibitors of fungal polygalacturonases and their use
control fungal disease
Patent: US 556980-A 5 29-OCT-1996;
Location/Qualifiers
1. .215
                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
                                                                                                                                   HTG
                                                                                                                                                                                                                                HUAC004787 216021 bp
Homo sapiens Chromosome
Adams,M.D., Loftus,B.J., Zhou,L., Crosby,M.,
                          Primates; Catarrhini;
1 (bases 1 to 216021)
                                                                                                          human
                                                                                                                                                                                                                   sequence
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Pred. No. 4.40e-06;
73; Mismatches 77
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Pred. No. 9.04e-15;
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US 5569830.
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BAC clone CIT987SK-A-952F10, complete
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                                                              Eutheria;
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Adams, M.D. and Loftus, B.J.

Direct Submission

AL Submitted (24-JUI-1998) The Institute for Genomic Research, 9712

Medical Center Dr., Rockville, MD 20850, USA

On Jul 24, 1998 this sequence version replaced gi:3241936.

Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA e-mail address: humgenetigr.org. The orientation of the sequence is from SP6 end to T7 end. Genes were identified by a combination of five methods including: XGRAIL (available by anonymous ftp from arthur epm.ornl gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.Edu/-chris/GENSCANN.html) searches of the complette sequence against a peptide database, and the Human gene index database at TIGR (http://www.tigr.org/tdb/hgi/hgi.html).

Genes without pepetide homolgy having spliced EST hits are termed 'Unknown gene product'. Genes encoding trakas are predicted by trakascan-SE (Sean Eddy, http://genome.wustl.edu/eddy/trakascan-SE/).

Location/qualifiers

Location/qualifiers
                                                       AGGAGTCTTTTCTGACAAATTCCTCCT 164
                                                                                                                                                                                                                                                                                                                       h 14.48;
Similarity 12.28;
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Adams, M.D. and Loftus, B.J.
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/db_xref="dbSTS:G04338"
51778 c 49172 g 53987 t
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75810. 175945
note="1674"
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JOURNAL Submitted (01-AUG-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157, Berkeley, CA 94720, U.S.A. COMMENT Sequence submitted by: DOE Joint Genome Institute. FEATURES Location/Qualifiers source /organism="Homo sapiens" /db_xref="taxon:9606" /map="5g" /clone="1193" /chromosome="5"		Db 905 THGNONTYYWYKCKAKYRVSNRSGVSRSGSGSGTDYTTSSDATYYCGTHARTGGTKVKG 963 : :::: :: :: :: : :	DCCUSSION Sequence 22 from patent US 5795961. ACCESSION AR024229 NID 93977523 VERSION AR024229.1 GI:3977523 VERSION AR024229.1 GI:3977523 VERSION AR024229.1 GI:3977523 VERSION AR024229.1 GI:3977523 KEYWORDS Unknown. ORCANISM Unknown. Unclassified. Unknown. VI Dases I to 965) AUTHORS Kitamura, K. TITLE Recombinant human anti-Lewis b antibodies JOURNAL Location/Oualifiers SOURCE 1, (base 1 to 265) AUTHORS SURCE 1, (base 1 to 965) FEATURES 1 D65 SOURCE 1, (base 1 to 965) AUTHORS AUTHORS AUTHORS 1 2 18-AUG-1998; FEATURES 1 1965 BASE COUNT 192 a 170 c 226 g 205 t 172 others ORGIGIN OUETY Match 13.5%; Score 31; DB 25; Length 955; Best Local Similarity 20.2%; Pred. No. 7.82e-05; Matches 24; Conservative 52; Mismatches 42; Indels 1; Gaps 1; Matches 24; Conservative 52; Mismatches 42; Indels 1; Gaps 1; Db 845 SVTAADTAVYYCVRGRSYDSDGGDYWGGTTVVSSHTVKDWTSSSSASVGDRVTTCRSST 904 SI S
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complement(35238 35331)
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complement(19943.
/rpt_family="Alu"
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complement(33670. .33785)
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complement(30401. 30536)
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complement(30682. 30733)
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29495. .29976
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32617. .32908
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complement/ceric
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23744. .23767
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23473. .23761
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AL Submitted (24-JUL-1998) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA On Jul 24, 1998 this sequence version replaced gi:3241936. Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20850, USA e-mail address: humgenetigr.org. The orientation of the sequence is from SP6 end to TP end. Genes were identified by a combination of five methods including: XGRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.Edu/-chris/GENSCANW.html)searches of the complete sequence against a peptide database, and the Human gene Index database at TIGR (http://www.tigr.org/tdb/hgi/hgi.html). Genes without pepetide homolgy having spliced EST hits are termed 'Unknown gene product'. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
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3 (bases 1 to 216021)
Adams,M.D. and Loftus,B.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 216021)
Adams, M.D. and Loftus, B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams,M.D., Loftus,B.J., Zhou,L., Crosby,M., Fuhrmann,J., Mason,T.M., Brandon,R., Kim,U.J., Kerlavage,A.R. and Venter,J.C. Homo sapiens Chromosome 16 BAC clone CIT9875K-A-952F10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 216021)
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AC004787.1 GI:3337381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUACO04787 216021 bp DNA PRI 24-JUL-1998 HOMO sapiens Chromosome 16 BAC clone CIT987SK-A-952F10, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(37595. .37654)
/note-"GRAIL 2 excellent exon, frame 0"
/note-"GRAIL 2 excellent exon, frame 0"
complement(join(38063. .38218,38462. .38578,38741. .3899
39071. .39205,39532. .39630,39935. .40048,40300. .40410,
40503. .40661,41868. .41972,42103. .42225,42492. .42569,
44379. .44507))
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/note="788-100% protein identity GenPept:U18937"
complement(38069. 38215)
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/db_xref="dbEST:AI025011"
36901. .37164
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/db_xref="dbSTS:G26554"
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Pred. No. 1.30e-03;
45; Mismatches 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 GAGGAATTTGTCAGAAAAGACTCCTTCAGCTTCAGTTGCAAAGTCATACCCCGGCCCTGTT 103
85 CCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTG-AAGGAGT 143
                              18
                              CNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSANYNYGGNNYGAAK 77
                                                                                                                                                                                                                                                                                                                                                                                                                         CCATGTGAG
                                                                                                                                                                                                                                                                                                              g1819054
128278.1
                                                                                                                                                    1 (bases 1 to 215)
Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use
control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
Location/Qualifiers
1. .215
                                                                                                                                                                                                                                                                                                                                      Sequence 5 from patent US 128278
                                                                                                                                                                                                                                                                                  Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 14.7%;
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                    128278
                                                        h 11.8%;
similarity 20.0%;
22; Conservative
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/note="16084, CHLC.GCT10802, C
/db_xref="absTs:c09703"
175810. .175945 CHLC.GCT15C04, C1
/note="16316, CHLC.GCT15C04, C1
/db_xref="absTs:c09935"
199463. .199572
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27765. .27872
/note="7766, STS1-cSRL-27g3-uA/cSRL-27g3-uz, Chr. -,
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/db_xref="taxon:9606"
/chromosome="16"
/map="#16q21-22"
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/note="7608, STS1-cSRL-24g1-uA/cSRL-24g1-uZ,
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8 c 25 g
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/db_xref="dbSTS:G04338"
51778 c 49172 g 53987 t
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14.7%;
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Pred. No. 1.30e-03;
60; Mismatches 50
                                                         Score 27; DB 25;
Pred. No. 1.98e-02;
42; Mismatches 45
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Best Local Similarity 15.6%;
Matches 22; Conservative
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                                         primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        850 DTAVYYCVRGRSYDSDGGDYWGGTTVTVSSHTVKDMTSSSSASVGDRVTTCRSSTTHGNG 909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  910 NTYYWYKGKAKYRVSNRSGVS 930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 THYYTHTNYSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSYGSSKTAM 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 GGTCAAGAGGAGGACAAGGGG 62
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AR024229
g3977523
AR024229.1
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U87256.1
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Wallace,T.Paul, Harris,W.J., Carr,F.J., Old,L.J., Welt,S. and
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1 (bases 1 to 1056)
Brusgaard,K., Shukri,N.M., Malchenko,S., Koroleva,I. and Lohi,O.
                                                                                                                                                                                                                                                                                                            Mustela vison
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U87256
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                                                                                                                                                                                         Animal Science, Blichersalle 
Location/Qualifiers
                                                                                                                                                                                                         Submitted (27-JAN-1997) Breeding and Genetics, Animal Science, Blichersalle K25, Tjele 8830,
                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                            American mink.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192
               /standard_name="1167F"
complement(300. .320)
/standard_name="1167R"
a 221 c 210 g 2:
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170 c 226 g
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1.965
                                                                       /note="primers: 1167F:
gaggatcttaccgctgttgag"
98. .119
                                                                                                                                                                                                                                                                                                                                                       GI:4099442
                                                                                                                                              /organism="Mustela vison"
/db_xref="taxon:9667"
                                                                                                                               chromosome="1"
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n GT dinucleotide repeat, chromosome 1q.
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Pred. No. 1.9Be-02;
59; Mismatches 60;
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                   225 t
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                   189 others
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Best Local Similarity 34.1%;
Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                           460 CARGRYTGYAAYTGYTCDMTYTAYSCYG 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                   400 GGRTCYGTYTTYCTYRTYTCYCABYTGTTTACCYTCTMBMCYMGSMDGYAYGDGACRDYR 459
                                                                                                                                                                                                                                                                                                                                           110
                                                                                                                                                                                                                                                                                                                                                                                                               50 GGGTCTGGGCTGCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      638 DKKSGSGDKSHCKSKRKYKWMDRYHBCKSMCA 669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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Local Similarity 12.0%;
hes 11; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent: JP 19923
TEIJIN LID
OS Hepatitis C
PN JP 19923498(
PD 04-DEC-1992
PF 29-MAY-1991
PI MORINAGA TSC
ICHIKAWA YATARO
PC C12N15/LO
CC strandedness
CC topology: Li
                  Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 60966)
                                                                                     Homo saplens
                                                                                                                                     HTG
                                                                                                                                                                                               AC003030
                                                                                                                                                                                                                                      Нопо
                                                                                                                                                    AC003030.1
                                                                                                                                                                                                                 complete
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E0407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOTINAGA,T., Chayama,K., Kumada,H. and Ichikawa,Y. NUCLEIC ACID FRAGMENT WITHIN ENVELOPE REGION OF HE AND METHOD FOR DETECTING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage;
Hepatitis C-like viruses.
                                                                                                            human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E04076.1 GI:21722
JP 1992349885-A/1.
                                                                                                                                                                                                      3030 60966 bp
sapiens chromosome
lete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus
JP 1992349885-A/1
04-DEC-1992
29-MAY-1991 JP 1991152169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MORINAGA TSUTAE, CHAYAMA KAZUAKI, KUMADA HIROMITSU,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  topology: Linear;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strandedness: Single;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C12N15/10, C12Q1/68, C12Q1/70//C12N15/11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding envelope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Organism="Hepatitis C virus"
/db_xref="taxon:11103"
93 c 107 g 85 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                    GI:4092821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25; DB 25;
Pred. No. 2.76e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48;
                                                                                                                                                                                                                        DNA PRI 06-JAN-1999
19, overlapping cosmids R29828 and F25496,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. No: 7.48e-02;
Mismatches 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 565;
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Map and sequence oriented from p telomere to centromere. This accession is comprised of overlapping cosmids R29828 (bases 1 to 40,974) and F25496 (bases 23,336 to 60,965). R29928 is separated from cosmid F25496 (bases 23,355 to the left by a sequence gap of approximately 14 kb, which is to be filled by sequencing a restriction fragment from cosmid R27236 (currently in progress). Cosmid F25496 is separated from cosmid R2736 (currently in progress) cosmid F25496 is separated from cosmid R2736 (currently in progress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (04-JAN-1999) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (28-OCT-1997) Human Genome Center, Joint Genome
Institute/ Lawrence Livermore National Laboratory, 7000 East Ave.,
Livermore, CA 94551, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lamerdin, J.E., McCready, P.M., Skowronski, E., Viswanathan, V., Burkhart-Schultz, K., Gordon, L., Dias, J., Ramirez, M., Stilwagen, S., Phan, H., Velasco, N., Do, L., Regala, W., Terry, A., Garnes, J., Danganan, L., Erler, A., Christensen, M., Georgescu, A., Avila, J., Liu, S., Attix, C., Andreise, T., Trankheim, M., Anico-Keller, G., Coefield, J., Duarte, S., Lucas, S., Bruce, R., Thomas, P., Quan, G., Kronmiller, B., Arellano, A., Sanders, C., Ow, D., Nolan, M., Trong, S., Sequence analysis of a 2 Mb contig in 19p12 between UBA52 and D198455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www-bio.llnl.gov/genome/genome.html.
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4 (bases 1 to 60966)
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/note-"DDS similarity to overlapping ESTs:-AA963316
UT-R-E1-gi-c-06-0-UI.sl UI-R-E1 Rattus norvegicus cDNA
clone UI-R-E1-gi-c-06-0-UI 3', (220. .237); 100%
identity.--AA893275 EST197078 Normalized rat kidney, Bento
Soares Rattus sp. cDNA clone RKIBE38 3' end; (240. .257);
                                                                                                            /rpt_family="AluJo" 5028. .5045
                                                                                                                                                                                                                                                                                                                                                                                                                               /map="19pl2 between UBA52 and D19S455."
/cell_line="UV5HL9-5B for F25496, and 5HL2-B for R29828"
/clone_lib="LL19NC02 (for E25496) and LL19NC03 (for R29828) chromosome 19-specific cosmid libraries"
/note="Cosmid libraries constructed at LLNL from flow-sorted chromosomes from human-hamster hybrid cell lines UV5HL9-5B and 5HL2-B, each of which carries chromosome 19 as its only human chromosome."
                                                                                                                                                                                                                          /note="predicted exon, program: grail2exons_human_1.3, frame: 2, quality: good, score: 51.000" complement(1477.1706)
                                                                                                                                                                                                  /rpt_family="AluJo"
2105. .2406
                                                                                                                                                                                                                                                                                                     complement(1148
                                                                                                                                                                                                                                                                                                                                              /rpt_family="Alux" 930. .1066
                                                                                                                                                                                                                                                                                                                  /rpt_family-"FLAM_C'
                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="AluJo"
530. .824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="R29828-F25496"
/chromosome="19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .60966
                                                                                                                                                                         _family="AluSp"
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/product="R29821"
/product="R29821"
/product="R29821"
/product="R29821"
/db_xref="pin_9410683"
/db_xref="pin_9410683"
/db_xref="GI:4106983"
/db_xref="GI:41069
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complement(5186. .5264)
frame: 0, quality: excellent, score: 86.000"
5432. .5497
foote-"DDS similarity to overlapping ESts:-AA963316
UI-R-E1-gi-c-06-0-UI.sl UI-R-E1 Rattus norvegicus cDNA
clone UI-R-E1-gi-c-06-0-UI 3'; (238. .303); 88%
identity.--AA893275 EST197078 Normalized rat kidney, Bento
Scares Rattus sp. cDNA clone RKIBE38 3' end; (258. .323);
88% identity."
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join(<5028. 5045,5432. .5497,6480. .6575,8155. .8249,
10156. 10183,10562. .10717,11845. .11991,12086. .12176,
13147. .13550,14614. .14679,18199. .18248,18465. .18542,
18635. .18746,23665. .23755,24574. .24709,37283. .37493)
/note="Hypothetical human protein (partial)"
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8480. 8769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"predicted exon, program: grail2exons_human_1.3, frame: 0, quality: excellent, score: 94.000-=DDS similarity to overlapping ESTs:-(8155. .827) AA963316 UT-R-E1-gi-c-06-0-UI.si UI-R-E1 Rattus norvegicus cDNA clone UI-R-E1- gi-c-06-0-UI 3'; (400. .482): 888 identity.--(8155. .824) AA93275 EST197078 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone RKIBE38 3' end; (420. .505); 85% identity."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"DDS similarity to overlapping ESTs:-AA963316
UT-R-E1-g1-C-06-0-UI-SI UT-R-E1 Rattus norvegicus CDNA
clone UII-R-E1-g1-c-06-0-UI 3', (304. 399); 898
identity.--AA893275 EST197078 Normalized rat kidney, Bento
Soares Rattus sp. CDNA Clone RKIBE38 3' end; (324. 419);
898 identity.--(6480. 6660) predicted exon, program;
898 identity.--(6480. 6660) predicted exon, program;
grall2exons_human_1.3, frame: 2, quality: excellent,
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/rpt_family="AluJo"
6480. .6575
                                                                                                                                                                                                                                                                                                                                                                     /rpt_family-"AluSx" 9197. .9493
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8778. .8837
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/note="predicted exon, program/note="predicted exon, predicted exon, pr
    /note="predicted exon. program: grail2exons_human_l.3,
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10562. .10721
                                                                                                                       /rpt_family="AluY"
10156. .10183
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ellent, score: 83.000"
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Best Local Similarity 85.7%;
Matches 30; Conservative
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N Sequence 1 from Patent W

A62989

g3716861

A62989.1 GI:3716861
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                                                                                                                                                                                                                                                                                                                                                                                       unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unidentified
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frame: 1, quality: excellent, score: 100.000"
11845 .11991
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20234. .20341
/rpt_family="AluJo/FLAM"
complement(20344. .20655)
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18465. 18542
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19929. .20226
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19632. .19928
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                 /organism="unidentified"
/db_xref="taxon:32644"
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Pred. No. 2.76e-01;
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Best Local Similarity 10.8%;
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                                                                                                HUMPFUCAS 3290 bp DNA PRI 08-JAN-1995
H.sapiens fucosidase pseudogene.
M80816
9189864
9189864
alpha-L-fucosidase; lysosomal hydrolase; lysosome; pseudogene.
Homo sapiens DNA.
Homo sapiens DNA.
Eukarvok-----
Eukarvok----
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3290)
Seo.H.C., Willems, P.J., Kretz, K.A., Martin, B.M. and O'Brien, J.S. Fucosidosis; four new mutations and a new polymorphism Hum. Mol. Genet. 2 (4), 423-429 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (27-JAN-1997) Breeding and Genetics, Danish Institute of Animal Science, Blichersalle K25, Tjele 8830, DK Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.

(bases I to 1056)
Brusgaard, K., Shukri, N.M., Malchenko, S., Koroleva, I. and Lohi, O.
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Mustela vison GT dinucleotide repeat, chromosome 1q.
U87256
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complement(300. .320)
/standard_name="1167R"
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gaggatcttaccgctgttgag"
98. .119
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Pred. No. 9.88e-01;
40; Mismatches 17;
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Pred. No. 9.88e-01;
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Best Local Similarity 79.5%;
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                                                                                                                     chromosome 2.
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/db_xref="taxon:9606"
/map="7q31"
735. 2761
/gene="FUCA1P"
735. .2761
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a 660 c
                                                                                                                                                                            /gene="FUCA1P"
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                                                        Score 23; DB 29; Lo
Pred. No. 3.44e+00;
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8.25e127 3.13e-08 3.13e-08 3.13e-08 1.12e-07 5.71e-05 5.71e-05 5.71e-05 1.93e-04	t being printed,	7:part7 1:part13 23 28 88 88 88 88						AGGGACCA 229	98 Seconds cell updates/sec	algorithm	•	1_1 (TM)	<u>-</u> '		**
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useful in the production, gene of 178pp; English. Ide sequence of CD19gion (also Claime) in (see W84498). In (see W84498). In the comman of th	NTRE.	cDNA to mRNA; 439 BP. rst entry) rcinoma cDNA clone HP104 otein; HP10408; human; s Location/Qualifiers 75311 /*tag= a /note= "cDNA comprising the stop codon)	ALIGNMENTS	V63020	N71302 V63022		V63027 V63315 V63312	T13610 T76219 V44650 T76452 T76445 T05628			T76438 Q70466 Q70473 Q70473	Q70469 Q51787 Q51772	Q70466 T76363	Q70469 Q70465 Q70465	Q70468 Q70467 Q70465
nces - useful in the preparation of antibodies and teein production, gene diagnosis, and gene therapy 35; 178pp; English. Ing region (also claimed) for a novel human protein (see w88498). The clone was isolated from cDNA library using a signal sequence detection protein synthesis by in vitro translation. The has a putative signal sequence and a putative embrane domain. The invention provides nucleotide v84359-75) coding for 18 transmembrane proteins	03-JUN-1998; J02445. 03-JUN-1997; JP-144948. (PRDT-) PRDTEGENE INC. (SAGA) SAGAMI CHEM RES CENTRE. Kato S, Sekine S, Yamaguchi T; WPI: 99-045730/04. P-PSDB: W86498.	d; cDNA to mRNA; 439 BP. first entry) carcinoma cDNA clone HP10408. protein; HP10408; human; stomach cancer; ds. Location/Qualifiers 7531 /*tag- a /note= "cDNA comprising the coding region (minus the stop codon) is claimed (Claim 3)"	S.		HSV-1 gB and surround D. immitis ankyrin nD	D. immitis ankyrin nD	nalayi ankyri eotide nBmAn eotide nDian	DC43 TSAR library gen Human IL5 antisense o Mammalian DNA replica Chymase antisense oli Substance P receptor ADP ribosylation fact	Ballast Constituent c DC43 TSAR library gen DC43 TSAR library gen	Generic DNA sequence Generic DNA sequence	Substance P antisense Generic DNA sequence Generic DNA sequence Generic DNA sequence	Generic DNA sequence Mixed Oligonucleotide Generic DNA sequence	DNA	DNA sequence DNA sequence DNA sequence DNA sequence	
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26-MAY-1992;
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N81164; standard; DNA; 204 BP.
N81164;
08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions;
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MKI4-A consists of nucleotides 5-95 of (051735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also 051735-45 and 051747-59.
See also 051735-45 and 051747-59.
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Oligonucleotide; DNA probe; r
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Random point mutations were introduced into the alpha fragment of Random point mutations were introduced into the alpha fragment of Random point mutations were introduced into the association of the stranded template and an oligonuclectide was hybridised to single stranded template and an oligonuclectide was hybridised to it to generate a popp of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the rempisfied and then molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system.

The sequence covers all 1/6 difft base substitutions, most of which occurred sligularly in any given mutant.

See also P80575.
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05-MAY-1988, 105163.
30-MAR-1987; US-034819.
03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
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by prepn of single stranded template, annealing a primer,
misincorporation, completion of molecules and screening.
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Introducing random point mutations into nucleic acods by prepn of single stranded template, annealing a primer, elong misincorporation, completion of molecules and screening. Disclosure; p; English.

Disclosure; p; English.

Random point mutations were introduced into the alpha fragment E.coil beta-galactosidase. The wild type sequence was obtained single stranded template and an olligonucleotide was hybridised it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The
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Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions;
Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 1; Le Pred. No. 3.13e-08; 59; Mismatches 46
                                                                                                                                                                                                                                                                                          Bamford J, Reinikainen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46;
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RESULT RE
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Best Local 9
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Best Local :
                                                                                                                                                                                                                                                                      ULT 6
Q70470 standard; I
Q70470;
IO-APR-1995 (firs
WO9418318-A.
18-AUG-1994.
01-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
EP-571911-A.
01-DEC-1993.
01-DEC-1993; 108325.
24-MAY-1992; US-889651.
                                                                                                                                                                   Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding done effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide probe MKII-A consists of nucleotides 5-95 of (051735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also 051735-45 and 051747-59.

Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                 misc_feature
                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 93-378844/48.

New oligo:nucleotide probes specific for Mycobacteria - undetection and amplification of Mycobacteria nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q51746;
Q51746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    samples Claim 3; Page 14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shank DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide probe MKI4-A
Oligonucleotide; DNA probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BECT ) BECTON DICKINSON CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which occurred singularly in any given mutant.

See also P80575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146
                                                                                                                                                                                                                                                                                                                                                                                                                            11 ssvhsyyvvhvvshhhsvhhvhhvhvsvvvvhhvhvhvhhvhyhvyvsv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 ymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynv 145
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                                                                                                                                                                                                                                                                                                                                                                                                 CGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTGTTCCATGTGAGCTGCCAAGGAGGGTCAAGAGGAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hnhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvhc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCATAGGAGGAATTTGTCAGAAAAGACTCCTTCAGCTTCAGTTGCAAAGTCATACCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.7%;
larity 0.0%;
Conservative
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U00977
                                                                                                                                                                                                                                                                      (first entry)
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                                                                /*tag=
/note=
                                                                                                            Location/Qualifiers 55..60
                                                                                                                                                                                                                                                                                                                     DNA; 114
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7.9%;
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                                                                "encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91
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Pred.
43; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37;
Pred. No.
54; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 C;
                                                             bу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
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                                                             8
                                                             (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 9; 1
. 1.12e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; I
3.13e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 т;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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but
                                                                                                                                                                                                                    domain;
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RESULT ID AC Q7 AC
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CO 70470 is a generic DNA sequence used to generate random TSAR (Totally CC Synthetic Affinity Reagenity) peptides. This generic formula can also be crepresented as follows: X(NB)4(CAC)(NB)4(CAC)(NB)8(Z(NB)6(CAC)(NB)8) CC (CAC)2(NB)9.

CC -(CAC)2(NB)9.

CC -(CAC)2(
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Best I
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                                                                                                                                                                   18-AUG-1994.
11-FEB-1994;
01-FEB-1993;
01-FEB-1993;
31-JAN-1994;
(UYNC-) UNIV
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30-DEC-1993; US-776500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NDRTH CARDL
FOWlkes DM, Kay BK;
WPI; 94-279739/34.
Identifying proteins or peptide(s) which bind a ligand - screening a recombinant vector library expressing fusion comprising a binding domain and an effector domain
                                                                                                                                    Fowlkes
WPI; 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domeffector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                           P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
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070467;
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                                                                                                           94-279739/34.
DB; R65153.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R58378
                                                                                                                                                               US-176500.
US-176500.
US-189331.
US-189331.
V NDRTH CARDLINA.
Kay BK;
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                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/note= "this sequence represents'/2'; z
/note= "this sequence represents'/2'; z
sequence of 6, 9 or 12 nucleotides (see
comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 55..60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA; 114 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   direct and rapid detection in a screening : 5 \text{ A}; 10 \text{ C}; 0 \text{ G}; 0 \text{ T};
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 31;
Pred. No.
28; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; DB 12;
. 5.71e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     can
                                  proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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PS Disclosure; Page 35; 255pp; English.

CO 70467 is a generic DNA sequence used to generate random TSAR (Totally CC Synthetic Affinity Resquence used to generic formula can also be CC represented as follows: X(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)11. X CC and y are flanking restriction sites (X is not the same as Y) that are CC and y are flanking restriction sites (X is not the same as Y) that are CC and y appecified further. Other generic sequences are shown in 070466-68.

CC Other specific peptides generated by these generic sequences are shown in 070466-68.

CC comprising at least two functional regions - a binding domain with cC comprising at least two functional regions - a binding domain with cC chart the expressed peptide contains 2 or 4 cysteine residues positioned CC in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs CC confers some degree of conformational rigidity to the peptides. The TSARs CC conformational proteins comprising a TSAR binding domain can be used in vivo to CC radioisotope, peptide, toxin or enzyme, to the specific target or on the CC cannot can late the function of macromolecules. The TSARs complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing CC direct and rapid detection in a screening process.

Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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                                                                                                                                                                                                                                                                                                        W09418318-A.
18-AUG-1994: U00977.
01-FEB-1994: US-013416.
01-FEB-1993: US-013416.
30-DEC-1993: US-176500.
31-JAN-1994: US-189931.
(UYNC-) UNIV NORTH CAROLINA.
FOWLKES DM. KAY EK;
WPI; 94-779739/34.
P-PSDB; R65154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generic DNA sequence to generate a random TSAR peride library TSAR; totally synthetic affinity reagent; synthetic; binding of the synthetic concateneated heterofunctional protein; link effector domain; concateneated heterofunctional protein; link direct; rapid; detection; screening; treatment; generic; ss.
Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain Disclosure; Page 35; 255pp; English.

Q70466 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagants) peptides. This generic formula can also be represented as follows: X(NNB)11(TGC)(NNB)6Z(NNB)7(TGC)(NNB)10Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68.

Other specific peptides generated by these generic sequences are shown 1
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05-APR-1995
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Q70468 standard;
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/notc= "this sequence represents '2'; Z
sequence of 6, 9 or 12 nucleotides (see
comments)"
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Q70470 standa
Q70470;
10-APR-1995
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30; Mismatches 72
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pr identifying proteins or peptide(s) which bind a ligand - by pridentifying proteins or peptide(s) which bind a ligand - by proteins grant and an effector domain proteins proteins proteins processing a binding domain and an effector domain proteins grant proteins proteins
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01-FEB-1994; U00977.

01-FEB-1993; US-01341;

30-DEC-1993; US-17650;

31-DAN-1994; US-18630;

(UYNC-) UNIV NORTH CAL

FOWLKES DM, KAY BK;
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US-176500.
US-189331.
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RESULT RESULT OF THE PROPERTY 
                                        PT Identifying proteins or peptide(s) which bind a ligand - by precening a recombinant vector library expressing fusion proteins or per comprising a binding domain and an effector domain CC Q70468 is a generic DNA sequence used to generate random TSAR (Totally CC Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)11(TGC)(NNB)52(NNB)7(TGC)(NNB)10Y. X CC and Y are flanking restriction sites (X is not the same as Y) that are constructed by these generic sequences are shown in Q70466-68. CC other specified further. Other generic sequences are shown in Q70466-68. CC other specified peptides generated by these generic sequences are shown in Q70466-68. CC other specified periods generated by these generic sequences are shown in Q70466-68. CC comprising at least two functional regions - a binding domain with CC comprising at least two functional regions - a binding domain with the expressed peptide contains 2 or 4 cysteine residues positioned CC confer some degree of contains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned CC in, or flanking, the unpredicted or variant residues. These residues or compsis. Comprising a TSAR binding domain can be used in vivo to CC radioisotope, peptide, toxin or enzyme, to the specific target or on the monoclonal or polyclonal antibodies and therefore circumvent the need CC complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity Sequence 114 Bp; 0 A; 2 C; 2 G; 2 T;
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01 FEB-1993; US-013416.

30 DEC-1993; US-176500.

31 JAN-1994; US-189331.

(UYNC-) UNIV NORTH CAROLI

FOWIKES DM, Kay BK;

WPI; 94-279739/34.
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070468;
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/note= *this sequence represents '2'; 2
sequence of 6, 9 or 12 nucleotides (see
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74 89

9

Matches Ouery Match Best Local

Local

Similarity

12.7%; ilarity 3.0%; Conservative

Score Pred. 29; M

6.43e-04; DB 12;

Length 114;

Mismatches No.

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RESULT
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05-APR-1995
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US-189331.
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/note= "this sequence represents 'z'; z
sequence of 6, 9 or 12 nucleotides (see
comments)"
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070465;
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18-AUG-1994.
01-FEB-1994: U00977.
01-FEB-1993: US-013416.
01-FEB-1993: US-176500.
31-JAN-1994: US-189331.
(UYNC-) UNIV NORTH CAROLI
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LT 13
Q70469
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                                                                                                                                      CCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCCTCTTGACCCTCC 86
   standard;
                                                                                                                                                                                                    h 12.7%;
Similarity 2.1%;
2; Conservative
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/note= "this sequence represents '2'; Z can
sequence of 6, 9 or 12 nucleotides (see
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                                                                                                                                                                                                        Pred.
29; 1
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No. 6.43e-04
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RESULT
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CC (70466) is a generic DNA sequence used to generate random TSAR peptide
CC (19CC) (NNB)2(TGC)(NNB)14(TGC)Y X and Y are flanking restriction
CC (19CC) (NNB)5Z(NNB)2(TGC)(NNB)14(TGC)Y X and Y are flanking restriction
CC sites (X is not the same as Y) that are not specified further. This
CC sequence generates peptides that are cloverleaf in structure. Other
CC generic sequences are shown in 70465-58. Other specific peptides
CC generated by these generic sequences are shown in R65150-54. TSARs are
CC concatenated heterofunctional proteins or peptides, comprising at least
CC two functional regions - a binding domain with affinity for a ligand and
CC active. They may further comprise a linker peptide between the 2 domains.
CC The oligonuclostides are also designed so that the expressed peptide
CC contains 2 or 4 cysteine residues. These residues confer some degree of
CC unpredicted or variant residues. These residues confer some degree of
CC conformational rigidity to the peptides. The TSARs or comprising
CC at TSAR binding domain can be used in vivo to deliver a chemically or
CC biologically active molety, eg. metal ion, radioisotope, peptide, toxin
CC or enzyme, to the specific target or on the cell. They can also replace
CC and therefore circumvent the need for complex methods of hybridoma
CC conformation or in vivo antibody production. The TSARs are easily
CC characterised and have designed activity allowing direct and rapid
CC characterised and sarreenland activity allowing direct and rapid
                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local
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01-FEB-1993; US-013416.
01-FEB-1993; US-176500.
30-DEC-1993; US-189331.
31-JAN-1994; US-189331.
(UXNC-) UNIV NORTH CAROLI
FOWLKES DM, KBY, BK;
WPI; 94-279739/34.
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07-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR peptide librar TSAR; totally synthetic affilnity reagent; synthetic; binding effector domain; concateneated heterofunctional protein; link concateneated heterofunctional protein; link concateneated heterofunctional protein; so.
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Q70465 standa
Q70465;
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Synthetic.
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07-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain bisclosure; Page 35; 255pp; English.
             Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding deffector domain; concateneated heterofunctional protein; linke direct; rapid; detection; screening; treatment; generic; ss.
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114 BP; 0 A;
                                                                                            (first entry)
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                                                                                                                              DNA; 114
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Pred. No. 6
29; Mismat
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Mismatches 75
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RESULT TO DE LITER OF THE PRINCE OF THE PRIN
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Best Local Similarity 3.6%;
Matches 4; Conservative
                                          Synthetic.

W09440162-A1.

19-DEC-1996.
06-JUN-1996; U09306.
07-JUN-1995; US-474497.
(UTEC-) UNIV EAST CAROLINA.
Metzger WJ, NYCE JW;
WPI; 97-0518/1/05.
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOW1kes DM, Kay BK;
WPI: 94-279739/34.
                                                                                                                                                                                                                                                                                                                   Human endothelin-1 antisénse oligonucleotide.
Asthma; airway epithelium; adenosine free; cystic fibrosis;
chronic obstructive pulmonary disease; bronchitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 15
T76405 standard; DNA; 178
Treatment of airway diseases such as asthma - by topically applying
                                                                                                                                                                                                                                                                                                                                                                                                                                          l5-SEP-1997 (first entry)
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sequence of 6, 9 or 12 nucleotides (see
comments)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28; DB 12;
Pred. No. 2.12e-03
30; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 114;
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PT subject
PS Claim 5; Page 38: 71pp; English.
CC A method for treating airway disease in a subject has been produced,
CC A method for treating airway disease in a subject has been produced,
CC which involves the topical administration of an essentially adenosine
CC free antisense oligonucleotide (ON) to the airway epithelium of the
CC subject. The present sequence is an antisense oligonucleotide specific
CC for the human endothelin-1, targeted at the initiation codon. The
CC method can be used to treat airway diseases such as cystic fibrosis,
CC asthma, chronic obstructive pulmonary disease, bronchitis and other
CC airway diseases characterised by an inflammatory response. By
CC eliminating adenosine from the antisense oN, its liberation upon
CC antisense degradation is prevented, thereby preventing adenosine-
CC induced bronchoconstriction in patients with hyper-reactive airways.
CC Sequence 178 BP; O A; 52 C; 46 G; 32 T;
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                                                                                                                                                                                                                                                                                                     Matches
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114 GTATGACTTTGC 125
                                                                                                                      100 cttggcbbgccbcbbbcbgcbgbgbbbbtcbtgbgcbbbtbbtccbttctgbbbbbbb 159
                                                   160
                                                                                      54 CTGGGCTGCCCCTTGTCCTCCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGG 113
                                                                                                                                                                                            Match 12.2%;
Local Similarity 25.0%;
les 18; Conservative
                                             gggbtcbbbbbbc 171
                                                                                                                                                                                       Score 28; DB 32; Le Pred. No. 2.12e-03; 32; Mismatches 22;
                                                                                                                                                                                         0
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Search completed: Sun Oct 24 17:08:37 1999 Job time: 76 secs.

	-4.	

如果她也有不知识的,我们也是我们的,我们的,我们的的,我们的,我们的,我们的,我们的人,我们的人的人的人,我们的人的人,我们的人们的人,我们的人们的人们的人们的人	

***	(мт)

Release 3.1A John F. collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Tabular output not generated. MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm Sun Oct 24 17:08:54 1999; MasPar time 20.47 Seconds 967.578 Million cell updates/sec

N.A. Sequence: Comp: Scoring table: Description: Perfect Score: TABLE default Gap 6 (1-229) from US09092296.seq >US-09-092-296-2 1 ACCGGGACTTCAGTGTCTCC.......CCATCTCCCTTCAGGGACCA 229
TGGCCCTGAAGTCACAGAGG......GGTAGAGGGAAGTCCCTGGT

165359 seqs, 43243793 bases x 2

Nmatch

STD:

Dbase 0; Query 0

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: n-issued

Statistics: Mean 7.362; Variance 4.165; scale 1.768 1:5A_COMB 2:5B_COMB 3:5C_COMB 4:PCT9_COMB 5:backfiles1

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		ouerv			SUMMARLES			
No.	Score		Length	DB	ID	Description	ď	Pred. No.
1	46	20.1	7218	2	US-08-232-	Seguence 14	- 1	370-1
c 2	33	14.4	215	_	8	л ;		0.070 E0
ω	31	ا <u>ا</u>	570	u F	182-88-88-) (- 0	6.3be-08
) ح) (11.	200	. ر	00-00-580-	sequence 22, 2		1.05e-06
1 #	2/	11.8	215	_	US-08-238-	Sequence 5, A	O	2.44e-04
0	27	11.8	965	ω	US-08-388-	22.		
O	22	9.6	75	4	PCT-US95-1	9 1	٠. ,	7.4.0.01
c 7	22		18	4	PCT-US95-1	98	Applicati	1 540-01
8	22	•	82	4	PCT-US95-1	97	Applicati	5/0-01
0	22		3088	ω	US-08-418-	1		1 540-01
c 10	12		65	_	US-08-471-	145	licat	276-01
II	21		6 6	_	US-08-471-		Applicat	5 276-01
c 12	21		68	_	US-08-471-			
13	22	9.2	69	۳	US-08-471-			5.27e-01
. L	21		74	4	PCT-US95-1	94,		5.276-01
	21	٠	74	4	PCT-US95-1	100,	7	5.27e-01
_	21	٠	75	4	PCT-US95-1	99.		
17	21		81	4	PCT-US95-1	98	٠.,	. i
Σ	21		81	4	PCT-US95-1	92	1	7 270-01
c 19	21		83	4	DOT - 11505 - 1	3 1	٠,	
20	2	ء د	5 1	٠,	1000000	, ,	Applicati	0.2/e-UL
	N	9.2	3.2	Ú	05-08-353-	Sequence 16, F	Applicati :	5.27e-01

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45	44	43	42	41	40	9	8 8	37	36	35	34	ω	32	31	30	29	2	27	20	2.5	24	2 6	2 6	2 1
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8.7	9.2	9.2	9.2	9.2	9.2	9.2	9.2	9.2	9.2	9.2	9.2	9.2	9.2	9.2	9.2	9.2	9.2	9.2	9.2	9.2	9.2	2		9.2
66	5503	5503	5503	5503	5235	5235	5235	5235	911	911	911	911	909	909	909	909	908	908	908	908	906	906	906	906
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PCT-US95-1	US-09-031-	US-08-847-	US-08-847-	US-09-031-	US-09-031-	US-08-847-	US-08-847-	US-09-031-	US-09-031-	US-08-847-	US-08-847-	US-09-031-	US-08-847-	US-09-031-	US-08-847-	us-09-031-	US-09-031-	US-08-847-	US-08-847-	US-09-031-	US-09-031-	US-08-847-	US-08-847-	
		Sequence 32					Sequence 36,				Sequence 24,			Sequence 25,				Sequence 37,		Sequence 39		Sequence 40,	Sequence 41,	Sequence 41
•	Applicati	-	-		, Applicati		, Applicati					Applicati		Applicati			, Applicati	-	-	-	-	, Applicati	•	, Applicati
	5 276-01		5.27e-01	. 27e			5.27e-01				5.27e-01			276			. 27€	. 276	. 27e	276	. 27€	-	. 27e	5.27e-01

ALIGNMENTS

COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER STATE: FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: PATENTIN Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION NUMBER: US/07/935,313.
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 30472/114 IMMU
TELEPHONE: (703)836-9300
TELEFAX: (703)83-4109
TELEFAX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS: Sequence 14, Application US/08232463 Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION: US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP. XXXXXX APPLICANT: DORNER, F.
APPLICANT: SCHELFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS: STREET: 1800 CITY: Alexandria STATE: VA ADDRESSEE: E: Foley & Lardner 1800 Diagonal Road, Suite 500 #1.25

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RESULT
ID U
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 7218 base pairs
TYPE: nucletc acid
STRANDEDNESS: single
TOPOLOGY: linear
INMEDIATE SOURCE:
CLONE: pTzgpt-PIs
SEOUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 2307
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Patent No. 5569830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-238-163-5 STANDARD; DNA; UNC; 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 CTTGAAAAGTCTGCCTCCTCCATCTCCCTTCAGGGACCA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 CTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 GTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.1%;
Local Similarity 2.3%;
es 5; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 CTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTT 67
                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend khourie and Crew
STREFT: Steuart Street Tower, One Market Plaza
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LABAVITCH, John M. APPLICANT: POWELL, Ann APPLICANT: STOTZ, Henrik
                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 03-MAY CLASSIFICATION: 800
                                                                                                                                                                                                                                                                    COUNTRY: US
ZIP: 94105-1493
        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative 129; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                             California
                                                                                                                                                                                                                                                                                                                                                                                                                                 BENNETT, Alan
                                                                                                                                                                     03-MAY-1994
                                                                                                                                                                                   US/08/238,163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46; DB 2;
Pred. No. 3.37e-16
                                                                                                           2307E-540
                                                                                                                                                                                                          Version
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                                    STRANDEDNESS:
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LOCATION: 1..215
OTHER INFORMATION: /standard_name- "Deduced an
OTHER INFORMATION: sequence of PGIP from bean.
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
US-08-388-672A-22 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                      126 TGCAAAGTCATACCCGGCCCTGTTCCATGTGAGCTGCCAAGGAGGTCAAGAGGAGGACA 67
                                                                                                                                                                                                                                                                                                                                                           185 ATTCCAGGAAGCTGGACTCATAGGAGGAATTTGTCAGAAAAGACTCCTTCAGCTTC-AGT 127
                                                                                                                                                                          120 YGSSKTAMTSRNRTGKTANNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGSKNNGDR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 14.4%; Score 33; DB 1; Length 215;
Local Similarity 14.6%; Pred. No. 6.36e-08;
hes 26; Conservative 73; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                  61 YSSANYNYGGNNVGAAKTHYYTHTNVSGADSKTVTDSYNASGTSSSNGGTD-GNRSGADS 119
                                                                                                                                                                                                                                                                                                                                                                                                                       1 MTNVTMSSSSVVSRTASCNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
FEATURE:
                                                                                                                     AGGGGCAGCCCAGACCCCATAGTGGCCACTGCGCTCCTGGGATGGAGGAGACACTGAA
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   965
   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Sequence 22, Application US/08388672A Sequence 22, Application US/08388672A Patent No. 5795961 APPLICANT: INFORMATION: Old, Lloyd J. Carr, Frank J. Harris, William Wallace, Sydney T. Paul 4

Kunio

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA: CORRESPONDENCE ADDRESS NUMBER OF SEQUENCES: TITLE OF INVENTION: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS STATE: New York COUNTRY: U.S.A. CITY: New York STREET: ZIP: 10022 ADDRESSEE: 805 Third Avenue Felfe and Lynch Recombinant Human Anti-Lewis Antibodies 25 Release #1.0, Version #1

INFORMATION FOR SEQ ID NO: ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5795961man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 54
TELECOMMUNICATION INFORMATION: SEQUENCE CHARACTERISTICS TYPE: nucleic acid TELEPHONE: CLASSIFICATION: FILING DATE: APPLICATION NUMBER: 212-838-3884 212-688-9200 14-FEB-1995 US/08/388,672 LUD 5409

TOPOLOGY: unknown MOLECULE TYPE: DNA (genomic) SEQUENCE 965 BP; 192 A; 170 C; 2 226 G; 200 T; 177

unknown

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                                             Ouery Match 11.8%;
Best Local Similarity 20.0%;
Matches 22; Conservative
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-9600
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                   NAME/KEY: misc_feature
LOCATION: 1..215
OTHER INFORMATION: /standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-238-163-5 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08238163 Sequence 5, Application US/08238163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             845 SYTAADTAVYYCVRGRSYDSDGGDYWGGTTVTVSSHUVKDMTSSSSASVGDRVTTCRSST 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90s THGNGNTYYWYKGKAKYRVSNRSGVSRSGSGSGTDYTTSSDATYYCGTHARTGGTKVKG
    85
                         18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 GACC-CTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 CCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCCTCTT 78
                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 03-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BENNETT, Alan APPLICANT: LABAVITCH, John M. APPLICANT: POWELL, Ann APPLICANT: STOTZ, Henrik
                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TIPLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
NUMBER OF SEQUENCES: 24
                                                                                                                                               FEATURE:
                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
CCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTG-AAGGAGT 143
                     CNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSANYNYGGNNVGAAK 77
                                                                                                                                                                                                                                                                 NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 23
                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
23; Conse
                                                                                                                                                                                                                                                                                                                                                                                                               94105-1493
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ilarity 19.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     California
                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Townsend and Townsend Khourie and Crew
Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                   US/08/238,163
                                           Score 27; DB 1;
Pred. NO. 2.44e-04
42; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 3; I
Pred. No. 1.05e-06;
53; Mismatches 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215
                                                               DB 1; Length 215;
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RESULT
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-388-672A-22 STANDARD;
                                                                                                                                                                                                                                                                                   TELEPHONE: 212-688-92
TELEFAX: 212-B38-3884
INFORMATION FOR SEQ ID NO:
                                                                                                                                                             y Match 11.8%;
Local Similarity 15.6%;
hes 22; Conservative
                                82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 THYYTHTNVSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSYGSSKTAM 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: Felfe and
                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 965 base pairs
                                                                                                                                                                                                                             TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: unk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 805 Third
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                               GGTCAAGAGGAGACAAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMA'
                                                                                                                                                                                                                               unknown
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                                                                                                                                                                                                                                          unknown
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MOLECULE TYPE: DNA (genomic) SEQUENCE 965 BP; 192 A; 170 C; 226 G; 200 T; 177 OTHER.
                                                                                           850 DTAVYYCVRGRSYDSDGGDYWGGTTVTVSSHUVKDMTSSSSASVGDRVTTCRSSTTHGNG 909
910 NTYYWYKGKAKYRVSNRSGVS 930
                                                                                                                                           202 GCCAGACTTTTCAAGCAATTCCAGGAAGCTGGACTCATAGGAGGAATTTGTCAGAAAAGA 143
                                                                                                                                                                                           790 GGVRSTSTCTASDYTTSYWGWVRGRGWGDYGGGYTNYNGKRGRVTMADTSSNSRSSVTAA 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 CTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5795961man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5409
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,672A
FILING DATE: 14-FEB-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Welt, Sydney
APPLICANT: Kitamura, Kunio
TITLE OF INVENTION: Recombinant Human Anti-Lewis
TITLE OF INVENTION: Antibodies
                                             CTCCTTCAGCTTCAGTTGCAAAGTCATACCCGGCCCTGTTCCATGTGAGCTGCCAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

    Application US/08388672A
    Application US/08388672A
    5795961

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harris, William J.
Carr, Frank J.
Old, Lloyd J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Felfe and Lynch
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                                                                                                                                                                                                                                              Score 27; DB 3; Len Pred. No. 2.44e-04; 59; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 75 BP; 1 A; 1 C; 7 G; 5 T; 61 OTHER.
                                                                                                            Sequence 98, Application PC/TUS9511934
Sequence 98, Application PC/TUS9511934
GRMERAL INFORMATION:
APPLICANT: Cytogen Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Ver:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US95-11934-99 STANDARD; DNA; UNC; 75 BP
                                                                                                                                                                          XXXXX
                                                                                                                                                                                     PCT-US95-11934-98 STANDARD; DNA; UNC; 81
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEG ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
                                                                                                                                                                                                                                      110 CCGGGTATG 118
                                                                                                                                                                                                                                                             65 NBGGTTGTG 73
                                                                                                                                                                                                                                                                                     50 GGGTCTGGGCTGCCCCTTGTCCTCCTTGACCCTCCTTGGCAGCTCACATGGAACAGGG 109
                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 18,872
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9990
TELEFAX: (212) 90-
                                                    APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                            APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New
COUNTRY: US
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Misrock, S. L. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: singl
                                   STREET:
                                                ADDRESSEE:
                     T: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
            New York
                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                9.6%;
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                                                                                                                                                                                                                                                                                                                                    Score 22; DB 4; Length 75; Pred. No. 1.54e-01; 19; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1101-196-228
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Sequence 97, Application PC/TUS9511934
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           XXXXXX
                                   CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,8
          REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
  TELEPHONE:
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Query Match
Best Local Similarity
Matches 5; Conser
                                                                                                                                              TELEFAX: (212) 869-9741,
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
                                                                           MOLECULE TYPE: DNA (genomic)
SEQUENCE 81 BP; 6 A; 6 C; 4 G; 5 T; 60 OTHER
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FROM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                              TOPOLOGY: 1. MOLECULE TYPE:
                                                                                                                                                                                                                                                                                       NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                        TELEPHONE:
9.6%;
ilarity 7.6%;
Conservative
                                                                                                               linear
                                                                                                                                                                                                                                                                        (212)
                                                                                                                                    single
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Score 22: DB 4; I
Pred. No. 1.54e-01;
20; Mismatches 41
                                                                                                                                                                                                                 98:
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    41; Indels
                                     Length 81;
    0,
      0
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PCT-US95-11934-97 STANDARD; DNA; UNC; 82 ВP

TITLE OF INVENTION: Antigen Binding POTITLE OF INVENTION: Peptide Libraries NUMBER OF SEQUENCES: 103 CORRESPONDENCE ADDRESS: STREET: ADDRESSEE: E: Pennie & Edmonds 1155 Avenue of the Americas Cytogen Corporation Peptides (Abtides) From

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995 COUNTRY: New York 10036 USA

(212) 790-9090

1101-196-228

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Query Match
Best Local S
Matches
                             CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION MUMBER: JP HEI 6-71048
FILING DATE: 08 APPL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. $775688man F.
REGISTRATION NUMBER: 24618
REFERENCE/DOCKET NUMBER: 2589-024-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEEX: 24885 OPAT UR
TELEPENCE (703) 413-2220
TELEEX: 24885 OPAT UR
INFORMATION FOR SED ID NO: 1:
$500ENCE CHARACTERISTICS:
LENGTH: 3088 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 82 BP; 1 A; 2 C; 10 G; 8 T; 51 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08418444A Sequence 1, Application US/08418444A Patent No. 5773688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-418-444A-1 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 CCGGGTATG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 97:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 GGGTCTGGGCTGCCCCTTGTCCTCCTTGACCCTCCTTGGCAGCTCACATGGAACAGGG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,444A
FILING DATE: 07-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 NBGGTTGTG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KURODA, HISAO
APPLICANT: HIGOTA, NAOHIKO
APPLICANT: 1TO, KAZUTOSHI
TITLE OF INVENTION: GENE EXPRESSION VECTOR USING THE GENE
TITLE OF INVENTION: EXPRESSION REGULATING REGION OF THE ADP RIBOSYLATION
TITLE OF INVENTION: FACTOR
    MOLECULE TYPE:
                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 82 base pairs
                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                              STREET: 1755 S. CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                              22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.6%;
ilarity 8.7%;
Conservative
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                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                 OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT 55 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                      Floppy disk
  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 22; DB 4;
Pred. No. 1.54e-01
19; Mismatches 4
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US-08-471-052A-144 STANDARD; DNA; UNC; 66 BP.
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Query Match 9.6%;
Best Local Similarity 72.0%;
Matches 36; Conservative
                                                                                                                                                                                                                    MOLECULE TYPE: DNA SEQUENCE 65 BP; 3 A; 3 C; 3 G; 2 T; 54 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 145, Application US/08471052A
Sequence 145, Application US/08471052A
Patent No. 5625033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 3088 BP; 716 A; 761 C; 672 G; 939 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-471-052A-145 STANDARD;
                                                                                                                                                                                                                                                                                                                                                            REFERENCE/POCKET NUMBER: 18,872
REFERENCE/POCKET NUMBER: 1101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAN: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR THE TENNIE
114 ccc66 110
                                                                 174 CTGGACTCATAGGAGGAATTTGTCAGAAAAGACTCCTTCAGCTTCAGTTGCAAAGTCATA 115
                                     61 CCTGG 65
                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEO ID NO:
                                                                                                    Match 9.2%;
Local Similarity 13.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIF: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 CCAAGGAGGTCAAGAGGAGGACAAGGGGCAGCCCAGACCCCATAGTGGC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 CCGAAGATGGGCCAGAGGGGGCCAGGGGCTGCCCAGGCGCCCTGCTGCC
                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 65 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/471,052A FILING DATE: 06-JUNE-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                             TOPOLOGY: unknown
                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115S Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pennie & Edmonds
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Pred. No. 1.54e-01;
0; Mismatches 14
                                                                                                                                                              Score 21; DB 1; L
Pred. No. 5.27e-01;
                                                                                                                                              16; Mismatches
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                                                                                                                                              40;
                                                                                                                                                                                 Length 65;
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                                                                                                                                              Indels
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Query Match
Best Local :
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REFERENCE/DOCKET NUMBER: 1101
TELLECOMMUNICATION INFORMATION:
TELLEPHONE: 212 790-9090
TELLEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 144:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 bases
                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA SEQUENCE 66 BP; 2 A; 3 C; 4 G; 2 T; 55 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/471,052A
FILING DATE: 06-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 144, Application US/08471052A
Sequence 144, Application US/08471052A
Patent No. 5625033
                                                                                                                                                                            Sequence 143, Application US/08471052A Sequence 143, Application US/08471052A Patent No. 5625033
                                                                                                                                                                                                                                   US-08-471-052A-143 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                         GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 166
                                                                                                                                                                                                                                                                                                                          Local Similarity 5.2% nes 3; Conservative
                                                                                                                                                                                                                                                                               37 AGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCCTTGACCCTCCTTGGCAGC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kay, B. K.
APPLICANT: FOwlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 166
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                           CILL NC. STATE: NC. COUNTRY: U.S.A. COUNTRY: To: 10036-2711 TO: TOADABLE F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds
STREEF: 1155 Avenue of the Americas
CITY: New York
STATE: New York
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                                                                       STREET: 1155 AV
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                                                                                                   ADDRESSEE:
                                                                                      E: Pennie & Edmonds
1155 Avenue of the Americas
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5.28;
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Query Match
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Matches
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Sequence 142, Application US/08471052A
Patent NO. 5625033
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA
SEQUENCE 68 BP; 3 A; 3 C; 5 G; 3 T; 54 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XXXXX
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                TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 cccGG 110
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TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 143
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Local Similarity 13.8%;
hes 9; Conservative
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APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 68 bases
TYPE: nucleic acid
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REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,052A
FILING DATE: 06-JUNE-1995
                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPAT
OPERATING SYSTEM: PC-DO
SOFTWARE: PatentIn Rele
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                       REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790.9090
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ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/471,052A
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Y: U.S.A.
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1155 Avenue of the Americas
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N: 530
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Best Local
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Best Local
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP; 3 A; 4 C; 3 G; 1 T; 63 OTHER.
                      XXXXXX
                                   PCT-US95-11934-100 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA SEQUENCE 69 BP; 2 A; 4 C; 6 G; 2 T; 55 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 94, Application PC/TUS9511934
Sequence 94, Application PC/TUS9511934
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                       37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 18,872
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/RR64
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Local Similarity 5.2%;
local Simi
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Bir
TITLE OF INVENTION: Peptide Li
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CITY: New York
STATE: New York
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TYPE: nucleic acid
creanDEDNESS: single
                                                                                                                       GCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCCTCTTGACCCTCCTTGGCA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTGGCCACTATGGGGTCTGGCCTGGCCCCTTGTCCTCTTGACCCTCCTTGGCAGC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Misrock, S. Le REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US95/11934 FILING DATE: 20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: sinc
TOPOLOGY: unknown
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                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                           9.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigen Binding Peptides (Abtides) From Peptide Libraries
                                                                                                                                                                                                                       Score 21; DB 4;
Pred. No. 5.27e-01
20; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 21; DB 1; Leny...
Pred. No. 5.27e-01;
'A'smatches 37; Indels
                                        74 BP
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                                                                                                                                                                                                                                                                     Length 74;
                                                                                                                                                                                                                       Indels
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                                                                                                                                     Query Match
Best Local Similarity
Matches 5; Conser
                                                                                                                                                   TELEFAX: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 100:

SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs

TYPE: nucled: acid

STRANDEDNESS: single
                                                                                                                                MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP; 6 A; 6 C; 1 G; 1 T; 60 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 100, Application PC/TUS9511934
Sequence 100, Application PC/TUS9511934
GENERAL INFORMATION:
                                    121 AGTCATACCCGGCCCTGTTCCATGTGAGCTGCCAAGGAGGGTCAAGAGGAGGACAAGGGG 62
61 CAGCCCA 55
                    65 NACCACA 71
                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cytogen TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 20-SEI CLASSIFICATION:
                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                                                                         10036
                                                                                                                                                                                                                                                                                            Misrock,
                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytogen Corporation
VENTION: Antigen Binding Peptides (Abtides) From
VENTION: Peptide Libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pennie &
                                                                                                                                                                                                                                                                                                                            20-SEP-1995
                                                                                                9.2%;
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                                                                                     Score 21; DB 4; L
Pred. No. 5.27e-01;
19; Mismatches 43
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                                                                                     43;
                                                                                                          Length 74;
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Result Query NO. Score Match Length DB ID Description Pred. No. C 1 53 23.1 328 23 Al135523 UI-R-C2p-nq-e-02-0-UI. 4.59e-50 C 2 52 22.7 252 17 AA754459 97SN1787 Rice Immature 2.11e-48 C 3 50 21.8 252 17 AA754459 97SN1787 Rice Immature 4.11e-25 C 4 40 17.5 247 17 AA754458 97SN1784 Rice Immature 4.11e-29 C 5 32 14.0 247 17 AA754458 97SN1784 Rice Immature 4.11e-29 C 6 32 14.0 247 17 AA754458 97SN1784 Rice Immature 3.60e-17 C 7 11.8 2275 20 AF034173 AF034173 Human mRNA (T 3.60e-17 C 1 1.8 2275 20 AF034173 AF034173 Human mRNA (T 2.78e-10 C 2 3 10.0 238 12 AA376566 EST89915 HSC172 cells 3.12e-05 C 3 2 14.0 238 12 AA376566 EST8915 HSC172 cells 3.12e-05 C 4 2 5 2 5 2 6 5 6 5 6 5 6 5 6 5 6 6 6 6 7 6 7 6 7 6	Release 3.1A John F. Collins, Blocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Nolecular Ltd MPsrch_nn n.a. f.n.a. database search, using mith-Waterman algorithm Run on: Sum Oct 24 16:59:27 1999; MasPar time 446.22 Seconds Tabular output not generated. 11229) from US09092296.seq 1220-498 Million cell updates/Sec Perfect Scorce 299 1202-498 Million cell updates/Sec Tabular output not generated. 12	· · · · · · · · · · · · · · · · · · ·
FEATURES	MMEDIO ORGGINA AMEDIO ORGAGINA AMEDIO ORGGINA AMEDIO ORGGINA AMEDIO ORGANI AME	c 11
Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9555 Email: msoares@blue.weeg.uiowa.edu The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult Lung library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics Seq primer: M13 Forward. Location/Qualifiers	33 10.0 426 8 T15255 33 10.0 1287 20 AF038250 Cris855 lambdaZAPST RLC 3.12e- 23 10.0 1287 20 AF038250 AF038250 Human RNNA (T 3.12e- 23 9.6 398 B D40392 24 9.6 399 41 A0375965 HSC[1501] AF038250 Human RNNA (T 3.12e- 25 9.6 395 41 A0375965 HSC[1501] AF038250 Human RNNA (T 3.12e- 26 9.6 404 17 AA730403 RACCISSO HUMAN RNNA (T 3.12e- 27 9.6 433 34 W79098 Zd75h10.11 Soares_fecta 4.75e- 28 9.6 433 34 W79098 Zd75h10.11 Soares_fecta 4.75e- 29 9.6 433 34 W79098 Zd75h10.11 Soares_fecta 4.75e- 29 9.6 433 34 W79098 Zd75h10.11 Soares_fecta 4.75e- 29 9.6 433 34 W79098 Zd75h10.11 Soares_fecta 4.75e- 21 9.2 370 Z5 A1128672 WEST00055 Mixed stage, 6.60e- 21 9.2 410 Z A0444216 GSSTC0313 Trypenosoma 6.60e- 21 9.2 410 Z A0444216 GSSTC0313 Trypenosoma 6.60e- 21 9.2 440 Z A0444216 GSSTC0313 Trypenosoma 6.60e- 21 9.2 440 Z A044216 GSSTC0313 Trypenosoma 6.60e- 21 9.2 440 Z A044216 GSSTC0313 Trypenosoma 6.60e- 21 9.2 440 Z A04828673 WC46EBT7 Myceilal Neur 6.60e- 21 9.2 440 Z A089874 ZB73 Lambda-FBL2 Arab 6.60e- 21 9.2 440 Z A089874 ZB73 Lambda-FBL2 Arab 6.60e- 21 9.2 540 Z A0898768 WC46C7T7 Myceilal Neur 6.60e- 21 9.2 540 Z A0898768 WC46C7T7 Myceilal Neur 6.60e- 21 9.2 540 Z A0898768 WC46C7T7 Myceilal Neur 6.60e- 21 9.2 688 Z A0415674 ZB73 Lambda-FBL2 Arab 6.60e- 21 9.2 540 Z A0898768 WC46C7T7 Myceilal Neur 6.60e- 21 9.2 540 Z A0898768 WC46C7T7 Myceilal Neur 6.60e- 21 9.2 540 Z A0898768 WC46C7T7 Myceilal Neur 6.60e- 21 9.2 540 Z A0898768 WC46C7T7 Myceilal Neur 6.60e- 21 9.2 540 Z A0898768 WC46C7T7 Myceilal Neur 6.60e- 21 9.2 540 Z A0898768 WC46C7T7 Myceilal Neur 6.60e- 21 9.2 540 Z A0898768 WC46C7T7 Myceilal Neur 6.60e- 21 9.2 540 Z A0898768 WC46C7T7 Myceilal Neur 6.60e- 21 9.2 540 Z A0898768 WC46C7T7 Myceilal Neur 6.60e- 21 9.2 540 Z A0898768 WC46C7T7 Myceilal Neur 6.60e- 21 9.2 540 Z A0898768 WC46C7T7 Myceilal Neur 6.60e- 21 9.2 540 Z A0898768 WC46C7T7 Myceilal Neur 6.60e- 21 9.2 540 Z A0898768 WC46C7T7 Myceilal Neur 6.60e- 21 21 9.2 540 Z A0898768 WC46C7T7 Myceilal Neur 6.60e- 21 21 9.2 540 Z A0898768 WC46C7T7 Myceilal Neur 6.60e- 21	10.0 364 10.0 412

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 TGGTCCCCGGTGAGAGGTGGAGGAGGAGGCAGATCTTTTGGAGCATGTCCAGAAAGCCGG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 ACTCATAGGAGGAATTTGTCAGAAAAGACTCCTTCAGCTTCAGTTGCAAAGTCA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 TGGTCCCTGAAGGGAGGAGGAGGGAGGCAGA-CTTTTCAAGCAATTCCAGGAAGCTGG 171
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Suwon, ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA754459 252 bp mRNA EST 20-JAN-1998 97SNI787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1787, mRNA Sequence.
AA754459
   Department of Cytogenetics
National Inst. of Agri. Sc.
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
                                                                                                                                                                                                                                                              1 (bases 1 to 252)
Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P., Kim, M.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y., Lee, M.C. and Eun, M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST
                                                                                                                                                                           Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
On Jan 14, 1998 this sequence version replaced gi:1797457.
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa
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/notes*vector: pyragic pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI: The UI-R-C2p
library is a subtracted library derived from the UI-R-C1
library, which is a subtracted library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, 8. 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture. The subtracted library (UI-R-C2p) was
constructed as follows: PCR amplified cDNA inserts from
UI-R-C1 clones from which 3' ESTs had been derived was
used as a driver in a hybridization with the UI-R-C1
library in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library) was
purified by hydroxyapatite column chromatography,
purified by hydroxyapatite column chromatography
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
UI-R-C2p library. This procedure has been previously
described (Bonafdo, Lennon and Soares, Genome Research 6:
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llarity 75.4%;
Conservative
                                                                                                                 Eun M.Y
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/clone_lib="UI-R-C2p"
/clone_lib="UI-R-C2p"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B g 91 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     described (Bonaldo, Lennon and
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/note-"Vector: pT7T3D-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              791-806, 1996)"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53; DB 23; Core 50; Pred. No. 4.59e-50; Indels
                                                                and Tech,
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SOURCE
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                                                                   FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
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                                       source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 CCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 TCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCCTCTTGACCCT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 YBCHGNBVWVCVASHGNYMSVHNCTBRGTHCDCKNVNWSTMTWGTVNWBNVSGDWHYWBV 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                     Department of Cytogenetics
National Inst. of Agri. Sci. and Tecl
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Back Hie Nahm, Dept of E
University, Yongin, Korea. 449-728 b)
Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted by Baek Hie Nahm, Dept of Biological Science, Myongjl University, Yongin, Korea. 449–728 bhnahm@bioserver.myongjl.ac.kr Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA754459 252 bp mRNA E51 47 VVVVII 97SNI787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza Satlva cDNA clone 97SNI787, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                           Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
On Jan 14, 1998 this sequence version replaced gi:1797457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 252)
Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
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Oryza sativa
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Email: myeun@sun20.asti.re.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Poaceae;
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ilarity 11.9%;
Conservative
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/cultlvar="Milyang23"
/note="Yector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/note]; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="97SN1787"
/clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
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            /organism="Oryza sativa"
                                                                Location/Qualifiers
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pred. No. 2.11e-48;
87; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                   and Tech,
                                                                                                                          of Biological Science, Myongji
28 bhnahm@bioserver.myongji.ac.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 252;
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2; Gaps

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RESULT 2
LOCUS
DEFINITION

Ър ç B BASE COUNT ORIGIN

Matches

REFERENCE

SOURCE KEYWORDS VERSION UID ACCESSION

ORGANISM

COMMENT

TITLE JOURNAL

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Best Local Similarity Matches 21; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGAGGAATTTGTCAGAAAAGACTCCTTCAGCTTCAGTTGCAAAGTCATACCCGGCCCTG 105
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97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza
cDNA clone 97SN1784, mRNA sequence.
AA754458
                                                                                                                                                 Email: myeun@sun20.asti.re.kr

Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji

University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr

Seq primer: Mi3 Reverse primer.
                                                                                                                                                                                                                                         Department of Cytogenetics National Inst. of Agri. Sci. Suwon, Kyunggido, Korea Tel: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l (bases 1 to 247)

Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P., Kim, M.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y., Lee, M.C. and Eun, M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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                                                                                                                                                                                                                                                                                                                                                        Contact: Eun M.Y.
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/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional CDWA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
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/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli sOLR"
/lab_host="E. coli sOLR"
/lab_host="E. coli sOLR"
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                                                          /organism="Oryza sativa"
/cultivar="Milyang23"
                                                                                                                                   Location/Qualifiers
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200 104 142 164 82 BASE COUNT ORIGIN

Query Match

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KEYWORDS VERSION ACCESSION DEFINITION

REFERENCE AUTHORS

COMMENT

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FEATURES

source

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Query Match 17.5%;
Best Local Similarity 10.7%;
Matches 22; Conservative
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On Jan 14, 1998 this sequence version replaced di:1797455.
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AA754458.1
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97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza
CDNA clone 97SN1784, mRNA sequence.
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Oryza sativa
                                                                                                                                                                                                                                                               Submitted by Back Hie Nahm, Dept of Biological Science, Myongji University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
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1 (bases 1 to 247)
Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
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/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
16 c 21 g 34 t 169 others
                                                                        /organism="Oryza sativa"
/cultivar="Milyang23"
/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional CDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
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/map="6"
/clone="97SN1784"
/clone_lib="Rice Immature
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d. No. 4.11e-29;
d. no. 4.11e-39;
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Best Local Similarity 13.3%;
Matches 26; Conservative
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                              1540 TYYKSWSRWYWYTTYTYWYCWCCTSMKSASCAMMRWMGYMGSRSSRSYWGYWGSM 1594
                                                                                                      1480 RYKRWKRRKGRRKRWTGMYKRWYRAMMYAMCAMMACWWYYWKMRGMKKCWKYRKYKKYTS 1539
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185 TIGCTIGAAAAGICIG 200
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                                                                                                                                                               Local Similarity
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                                                                   ATGGAGGAGGAGGCAGACTTTTCAAGCAATTCCAGGAAGCTGGACTCATAGGAGGAATTT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2275)

Tripodis, N. and Ragoussis, J.

Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                                               Guys Hospital
7th floor, Guy's Tower, London
Email: nikos@nki.nl.
                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Tripodis, Nikos
Division of Medical and Molecular Genetics
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AF034173 Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA
clone ntcon2 contig, mRNA sequence.
AF034173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
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                                                                                                                                                                                                                                         438
                                                                                                                                              Conservative
                                                                                                                                                                                                                     /Organism-"Homo sapiens"
/db_xref-"taxon:9606"
/db_xref-"taxon:9606"
/map-"6p21.3"
/clone-"ntcon2 contig"
/clone-int-"Human mRNA (Tripodis and Ragoussis)"
/clone_lib-"Human mRNA 599 t 149 others
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//dev_stage="5 days after pollination"
//lab_host="B. coli soLR"
16 c 21 g 34 t 169 ot
                                                                                                                                                               14.0%;
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LOCUS
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       COMMENT
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MEDLINE
                                                                               TITLE
                                                                                                                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 ACCCTCCT 87
                                                                                                                                                                                                                                                                                                                                                                                               8
                     IMAGE: molecular integration of the analysis of the human genome and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
On Sep 21, 1992 this sequence version replaced gi:279286
                                                                                         Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 348)
Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pletu,G., Poullot,Y.,
Sebastiani-Kabaktchis,C. and Tessier,A.
                                                                                                                                                                                                                                                                   EST
                                                                                                                                                                                                                                                                                                                                   F06958 348 bp mRNA EST 20-FEB-1995
HSC1QC101 normalized infant brain cDNA Homo sapiens cDNA clone
C-19C10, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guys Hospital
7th floor, Guy's Tower, London
Email: nikos@nki.nl.
                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Tripodis, Nikos
Division of Medical and Molecular Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    boundary
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2045115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tripodis, N. and Ragoussis, J. Generation of a transcription map in the region centromeric to human MHC across the 6p21.2-6p21.
                                                                                                                                                                                                                                                                                   F06958.1
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1 (bass 1 to 2275)
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Similarity 16.2%;
11; Conservative
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/clone_lib="Human mRNA (Tripodis and Ragoussis)"
/ 619 c 470 g 599 t 149 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="6p21.3"
                                                                                                                                                                                                                                                                                   GI:672595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 27; DB 20;
Pred. No. 2.78e-10;
39; Mismatches 17
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.3 chromosomal
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sapiens cDNA
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ACCESSION
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Best Local Similarity 67.2%;
Matches 45; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukheria; Primates; Catarrhini; Hominidae; Homo.

El (bases 1 to 238)

Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (bases 1 to 238)

S Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, M.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Frichman, J.L., Geoghagen, N.S., Glodek, A., Gneim, C.L., Hanna, M.C., Hedblom, E., Hinkle, P. S.Jr., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palangues, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Moreno-Palangues, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shriby, R., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shriby, R., Phillips, C.A., Perrick, J.M., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrick, J.M., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrick, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hastings, G.A., Kozak, D.L., Kunsch, C., Hangjun, J., Li, H., Meissner, P. S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu,C., Yu,G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA376266 238 bp mrNA EST 21-APR-1997
EST89915 HSC172 Cells II Homo Sapiens CDNA 5' end, mRNA sequence
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High quality sequence stop: 150.
Location/Qualifiers
1. 348
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1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
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Single read.
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/note="organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NoII; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector: Clone library from B. Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"
/clone="c-1qc10"
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Pred. No. 1.90e-06;
0; M1smatches 22;
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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man Mai, C., Clayron, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geophagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.I., Mazmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.M., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
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EST26816
AA323964
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For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 311)
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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Cerebellum II Homo sapiens cDNA
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/cell_type="fibroblast"
/cell_line="HSC172 (60PDL)"
/dev_stage="fetal"
70 c 50 g 66 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Organ: lung; Vector: pBluescript SK-; Site_1: ECORI; Stie_2: XhOI"
/db_xref="raxon:9606"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W33870 364 bp mRNA EST 13-MAY-1996 mc56b03.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:352493 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
26; Conserved
                                                                                                                                                  Contact: Marra M/Mouse EST Project
Washi-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, NO 63108
Tel: 314 286 1800
                                                                                                                                                                                                                                                                 Unpublished (1996)
On May 18, 1995 this sequence version replaced gi:811194.
                                                                                                                                                                                                                                                                                                                                                       Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995) 96026280 on Apr 14, 1993 this sequence version replaced gi:693635.
                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 364)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
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                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        พ33870.1 GI:1315794
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                        Seq primer: ETPrimer
                                               MGI:224293
                                                                                                                                                                                                                                                                                                                  The Washu-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                           Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research
    quality sequence stop: 360
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ECORI; Site_2: xho!"
/db_xref="ATCC (inhost):124516"
/db_xref="taxon:9606"
/dlone_lib="Cerebellum II"
/tissue_type="cerebellum"
/dev_stage="adult"
a 110 c 74 g 64 t 4 others
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Pred. No. 3.12e-05;
0; Mismatches 3;
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TITLE
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Best Local Similarity
Matches 31; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
On Jan 9, 1998 this sequence version replaced g1:936203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA769782 412 bp mRNA EST 29-DEC-1998 ah71b05.sl Soares_testis_NHT Homo sapiens cDNA clone 1321041 3',
                                                                              Insert Length: 691 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amers
High quality sequence stop: 402.
Location/Qualifiers
                                                                                                                                                                                    CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausberg@nih.gov
CDNA_Library_Preparation: M. Bento Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 412)
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AA769782
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National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA769782.1
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/organism="Homo sapiens"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; lst strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M.Fatima Bonaldo. "
/db_xref-"taxon:10090"
/clone="IMAGE:352493"
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73 c 87 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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/dev_stage="13.5-14.5dpc total
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Pred. No. 3.12e-05;
0; Mismatches 8
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|bution information can bu
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Project (CGAP),

M. Fatima

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Best Local Similarity
Matches 45; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 GGAGACA 14
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Carnegie Institution, 290 Panama
Tel: 4153251521
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ricinus communis
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyliophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
Rosidae; Euphorbiales; Euphorbiaceae; Ricinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
T15255
                                                                                                                                                                                                                                                                                 Email: crs@andrew.stanford.edu Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                    Expressed sequence tags from developing castor seeds Plant Physiol. 108, 1141-1150 (1995)
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T15255.1 GT:688907
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Crs855 lambdaZAPST
                                                                                                                                                                                                                                                                                                                                                            Contact: Somerville CR
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ilarity 67.2%;
Conservative
                                 was reversed. Partial CDNA clones /db_xref="taxon:3988" /clone="pcrs855"
     /clone_lib="lambdaZAPST"
61 c 99 g 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT773 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "/clone-"1321041"
                                                                                                                                                                                                                                                    Location/Qualifiers
l. .426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"
78 c 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I
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                                                                                                                                                                                                                                                                                                                                                                                                                                        to 426)
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APST Ricinus communis cDNA clone pcrs855, mRNA
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Pred. No. 3.12e-05;
0; Mismatches 22
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VERSION KEYWORDS

SOURCE

ORGANISM

DEFINTTION RESULT

13

ACCESSION

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REFERENCE AUTHORS

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COMMENT

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277 CTTCAGTGTCAACAACCTGCTTGGAGCCCAGTGGCCAATATGG 319
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Te1: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST project
WashU-HHMI Mouse EST project
WashLington University School of Medicinep
4444 Porest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA498488 481 bp mRNA EST 01-JUL-1997 vh44b06.rl Barstead mouse pooled organs MPLRB4 Mus musculus cDNA clone IMAGE:889811 5' similar to gb:M30514 Mouse muscle nicotinic acetylcholine receptor gamma-subunit (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: -28m13 rev2 ET from High quality sequence stop: 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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larity 71.4%;
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                                                                                                                                                         /tissue_type="pooled organs"
/dev_stage="7 day"
                                                                                                                                                                                           /sex="mixed"
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                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="FVB/N"
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Search completed: Sun Oct 24 17:07:02 1999 Job time : 455 secs.
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                                                                                                                                                       109 GCCGGGTATGACTTTGCAACTGAAGCTGAAGGA 141
                                                                                                                   441 STCMTHYNCCDCKTCGSAGVTVNHHDWSMAGGA 473
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1 (bases 1 to 1287)

Tripodis,N. and Ragoussis,J.
Generation of a transcription map in the region immediately centromeric to human MHC across the 5p21.2-5p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF038250 1287 bp mRNA EST 30-MAR-1998 AF038250 Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA clone ntcon9, mRNA sequence.
AF038250
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Tripodis, Nikos
Division of Medical and Molecular Genetics
Guys Hospital
7th floor, Guy's Tower, London SE1 9RT, UK
Email: nikosenki.nl
Location/Qualifiers
1.1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             boundary
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2045085.
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AF038250.1 GI:2815880
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                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_yref="taxon:9606"
/map="6p21.3"
/clone="ntcon9"
/clone=lib="Human mRNA (Tripodis and Ragoussis)"
/clone_lib="Human mRNA (Tripodis and Ragoussis)"
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sun Oct 24 16:22:19 1999; MasPar time 475.19 Seconds 1394.147 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-09-092-296-1 (1-239) from US09092296.seq 238

N.A. Sequence: Comp: 1 GGCCACCGGGACTTCAGTGT......CCCTTCAGGGACCAGCGTCA 239 CCGGTGGCCCTGAAGTCACA......GGGAAGTCCCTGGTCGCAGT

Scoring table: TABLE default Gap 6

Nma tch

STD : Dbase 0; Query 0

646147 seqs, 1385953633 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: emb158

Database:

Statistics:

1:em_ba1 2:em_ba2 3:em_fun 4:em_htg 5:em_hum1 6:em_hum2
7:em_in 8:em_om 9:em_or 10:em_ov 11:em_pat 12:em_ph
13:em_pl 14:em_ro 15:em_ests 16:em_vi
genbankll1
17:gb_ba1 18:gb_ba2 19:gb_htg1 20:gb_htg2 21:gb_in1
22:gb_in2 23:gb_om 24:gb_ov 25:gb_pat 26:gb_ph 27:gb_pl
28:gb_pl2 29:gb_pr1 30:gb_pr2 31:gb_pr3 32:gb_ro
33:gb_st 34:gb_sts 35:gb_sy 36:gb_un 37:gb_vi

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 9.607; Variance 4.824; scale 1.991

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A62989	E04 076 AC003030	AR024229	HUAC004787	MVU87256	AC005369	AR024229	HUAC004787	128278	I66494	AC005937	ID	
Sequence 1 from Patent	gDNA encoding envelope	Sequence 22 from paten	Homo sapiens Chromosom	Mustela vison GT dinuc	Homo sapiens chromosom	Sequence 22 from paten	Homo sapiens Chromosom	Sequence 5 from patent	Sequence 14 from paten	Homo sapiens clone UWG	Description	
1.07e+00	3.00e-01	8.16e-02	5.63e-03	5.63e-03	1.43e-03	8.69e-05	4 91e-06	5.87e-08	2.10e-15	7.72e-65	Pred. No.	

All manually edited bases have been reduced to quality zero Quality levels above 40 are expected to have less than

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quence		ombe chromosome	Mus musculus mRNA for	Mus musculus gene for	doacac	Homo sapiens mRNA for	Mouse Chromosome 10 BA	Homo sapiens chromosom	Human DNA sequence ***	Homo sapiens 3p22-8 PA	Drosophila melanogaste	w	ING DRAFT SEC	o sapiens mRNA	musculus CDO (MUC4	mRNA for	in		Mus musculus Bak gene,	D.melanogaster synapto	Human (clone SY2/10) q	Trypanosoma cruzi mRNA	rom Paten	sapiens clone DJ	ens clo			H.sapiens fucosidase p	piens chron	MARCETA ATSON G. GING
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ALIGNMENTS

RESULT	1
LOCUS	AC005937 47323 bp DNA PRI 05-NOV-1998
DEFINITION	Homo sapiens clone UWGC:370M23.002 from 6p21, comp
ACCESSION	
NID	93845393
VERSION	ÅC005937.1 GI:3845393
KEYWORDS	
SOURCE	human.
ORGANISM	
	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
	Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 47323)
AUTHORS	Janer, M., Guillaudeux, T., Vu, Q., Kutyavin, T., Harter, H. and
77 77 77	GGTAGHT? D. E.
TOTTRNAT	Finally telegation and the number of the section
REMARK	Fred Hitchinson Cancer Research Conter
	The Clinical Research Division
	1100 Fairview Ave. N., P.O. Box 19024
REFERENCE	2 (haspes 1 to 47323)
	e (vacto + to filed)
AUTHORS	Geraghty, D.E. and Olson, M.V.
TITLE	Direct Submission
JOURNAL	Submitted (05-NOV-1998) Human Genome Center, University of
D ENG DY	Washington, Box 352145, Seattle, WA 98195, USA
XEMAKK	University of Washington Human Genome Center Box 352145 Seattle, WA 98195
	Contact: Daniel E. Geraghty (geraghty@fhcrc.org)
COMMENT	Overlapping Sequences:
	5': UWGC:370m23.013 (Genbank Accession: AC005530)
	3 : OMGC:Y0/CIL2 (Genbank Accession: ACOU4211)
	Sequence Quality Assessment:
	estimates computed by the Phrap assembly program.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence has been validated by Multiple Complete Digest Mapping. Comparison of the experimentally derived map digest fragments with sequence-predicted fragments is given below. Small fragments below a variable cutoff (approximately 400-600bp) are not mapped and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragment groups are separated by dashed lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
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complement(21287. .21895)
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22715. .22687
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33515. .33767
                                                                                                                                                                                                                                                 complement(6972.
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/db_xref="taxon:9606"
/chromosome="6"
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1. .47323
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Local Similarity 100.08;
hes 112; Conservative
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Dorner, F., Scheiflinger, F. and Falkner, F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
                                                                                                                                                          Unknown.
                                                                                                                                                                         Unknown.
                                                                                                                                                                                                                                                 Sequence 14 from patent
                                                                                                                                          Unclassified
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37372. .3
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/nocke-"clonal variation with 3' overlapping clone insertion of 17bp repeat"
11489 c 12284 g 11994 t
                /organism="unknown"
1491 c 1486 g
                                                           Location/Qualifiers
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Pred. No. 7.72e-65;
0; Mismatches 0;
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US 5670367
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                     368 others
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Matches Query Match Best Local

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Query Match 15.1%;
Best Local Similarity 14.7%;
Matches 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 CTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 ATTCCAGGAAGCTGGACTCATAGGAGGAATTTGTCAGAAAAGACTCCTTCAGCTTC-AGT 131
                                                                                                                                                                                                                                                                                       180 RYGTGTKSNV 189
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                                                                                                                                                                                                                                                                                                                         61 YSSANYNYGGNNVGAAKTHYYTHTNVSGADSKTVTDSYNASGTSSSNGGTD-GNRSGADS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 GTCCTCCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAA 131
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Homo sapiens
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Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.
Plant Inhibitors of fungal polygalacturonases and
control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5 from patent US 5569830. I28278
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8 c 25 g
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Pred. No. 5.87e-08;
77; Mismatches 83
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Pred. No. 2.10e-15;
                                                                                                                                   16 BAC clone CIT987SK-A-952F10, complete
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Best Local Similarity 12.2%;
Matches 18; Conservative
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    1556 AAAMAAMYTTYYWMMWYYKKWMYTCCT 1582
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On Jul 24, 1998 this sequence version replaced gi:3241936.
Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20850, USA e-mail address: humgenetigr.org. The orientation of the sequence is from 576 end to T7 end. Genes were identified by a combination of five methods including: XGRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genescan (Chris Burge, http://gnomic.stanford.Edu/-chris/GENSCANW.html)searches of the complete sequence against a peptide database, and the Human gene Index database at TIGR (http://www.tigr.org/tdb/hgi/hgi/html), Genes without pepetide homolgy having spliced E5T hits are termed 'Unknown gene product'. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE).
                                                                                                                        TCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCTCT 81
                                           TGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGA 141
                                                                                 GRAMMAAAWYYKRRSCMAWYYYMRGRARKTYYYMARRRGCARSYKKYMAMYWAAWTTWCA 1555
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2 (bases 1 to 216021)
2 (bases 1 to 216021)
Adams, M.D. and Loftus, B.J.
Direct Submission
Submitted (02-JUN-1998) The Institute for Genomic Research, 9712
Submitted (02-JUN-1998) The MD 20850, USA, Email:
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1 (bases 1 to 216021)

Adams, M.D., Loftus, B.J., Zhou, L., Crosby, M., Fuhrmann, J., Mason, T.M., Brandon, R., Kim, U.J., Kerlavage, A.R. and Venter, J.C. Homo sapiens Chromosome 16 BAC clone CIT987sK-A-952F10

Unpublished
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Adams, M.D. and Loftus, B.J.
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/db_xref="db5T5:604338"
151778 c 49172 g 53987 t 124 others
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175801. .175945
17601. .175945
/db_xref="dbsTs:G09703"
/db_xref="dbsTs:G09703"
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/db_xref="taxon:9606"
/chromosome="16"
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Pred. No. 4.91e-06;
72; Mismatches 57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 GACC-CTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 CCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCCTT 82
                         E 3 (bases 1 to 74371)

E Kimmerly, W., Bondoo, M., Cheng, J., Connolly, K.S., Gunning, K.M.,

Bavis, C.A., Kadner, K., Miguel, T., Pitluck, S., Pollard, M.,

Rojeski, H., Subramanian, S. and Martin, C.H.

Direct Submission

Listitute, Lawrence Berkeley National Laboratory, MS 74-157,

Berkeley, CA 94720, U.S.A.

Sequence submitted by:

DOE Joint Genome Institute.

Location/Qualifiers

rce

1. 74371
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Sequence
AR024229
g3977523
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 74371)

Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Radner,K., Miguel,T., Miller,C., Pilluck,S., Pollard,M., Rojeski,H., Subramanian,S. and Martin,C.H.

Sequencing of human chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant human anti-Lewis b antibodies Patent: US 5795961-A 22 18-AUG-1998; Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACO05369 74371 bp DNA PRI 01-AUG-1998 Homo sapiens chromosome 5, BAC clone 11933 (LBNL H175), complete
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Wallace,T.Paul, Harris,W.J., Carr,F.J., Old,L.J., Welt,S. and
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                                                                                                                                                                                                                                                                      Ricke, D.O.
                                                                                                                                                                                                                                                                                                  Unpublished
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170 c 226 g
l. ./43/1
/organism="Homo sapiens"
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Pred. No. 8.69e-05;
52; Mismatches 42
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                                                                                                                                                                                                                                /rpt_family="Ll"
14175, 14470
             complement(16675. .16977)
/rpt_family="Alu"
complement(16993. .17085)
/rpt_family="wER42"
complement(17678. .18276)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="Alu"
complement(7830. .8185)
/standard_name="possible repeat"
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5327. .5602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="Alu" 2818. .2859
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893. .1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/map="5q"
                                                                                                                                          /rpt_family="Alu"
16671, .16600
                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family-"Alu"
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/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(9740.
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                                                                                                                        16671. .16690
/note="(T)20"
                                                                                                                                                                                                      complement(14906.
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/note="(CA)19"
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/note-"(A)22"
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                                                                                         /rpt_type-tandem
/rpt_unit=T
                                                                                                                                                                            15300.
                                                                                                                                                                                                                      /rpt_family="Alu"
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/rpt_unit=AC
                                                                                                                                                                                                                                                                                                                     /note="(AC)12"
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13727. .13750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="Alu"
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t_unit=CA
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complement(31573. .31724)
/note="GRAIL 2 excellent exon, f;
complement(31159. .3223)
/note="GRAIL 2 excellent exon, f;
2388. .32488
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32617. .32908
              complement(33670. .33785)
/rpt_family="Alu"
complement(34021. .34144)
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complement(35238. .35331)
                                                                                                                                                                                                                                                                                                      /note="GRAIL 2 excellent exon, frame 2"
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complement(30401. .30536)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="Alu"
23473. .23761
                                                                                                                                                                                                                                                                                                                                                                                                                        'rpt_family="Alu"
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jOin(29485. .29559,29598. .29779)
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29495. .29976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(28769. .28838)
/note-"GRAIL 2 excellent exon, frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(25727
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complement/nenr
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23744. .23767
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complement(22638.
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21736. .22035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(19943.
/rpt_family="Alu"
                                                                                                             /rpt_family-"MLT1"
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19914. .19945
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19305. .19583
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4. .28057
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ORGANISM
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LOCUS
DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
JOURNAL
                                                                                                  Query Match 11.8%;
Best Local Similarity 12.8%;
                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.2%; Score 29; DB 31; Length 74371; Best Local Similarity 16.7%; Pred. No. 1.43e-03; Matches 14; Conservative 45; Mismatches 24; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15929 CNSRSKSKRGWGYRSWKKYRCAMWMTCKSS-KCWCWSYRMRMKCYSCSYCYCSSGKKYWC 15987
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                                     576 SCRHDVBMWSKWCWGKKSCCKSIGKDKMSGCAYCGKRMRRCSRYMMMRMCVGSGTWARCC 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 CCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGGCCACTATGGGGTCTGGGCTG 65
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Carnivora; Eissipedia; Mustelidae; Mustela.
1 (bases 1 to 1056)
Erusgaard,K., Shukri,N.M., Malchenko,S., Koroleva,I. and Lohi,O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g4099442
U87256.1
                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (27-JAN-1997) Breeding and Genetics, Danish Institute Animal Science, Blichersalle K25, Tjele 8830, DK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          American mink.
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U87256
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                                                                                  Conservative
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36592. 36663
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36901. 37222
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36901. 37164
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/standard_name="1167R"
a 221 c 210 g 22
                                                                                                                                                                                                                                                          /note="primers: 1167F: agcccctgcatatctacttctt, 1167R:
gaggatcttaccgctgttgag"
98. .119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="GRAIL 2 excellent exon, frame 0"
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44379...44507),
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/note="78%-100% protein identity GenPept:U18937"
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/db_xref="taxon:9667"
/chromosome-"1"
/map="1q"
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/db_xref="dbSTS:G26554"
complement(37595...37654)
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GT dinucleotide repeat, chromosome 1q.
                                                                             Score 28; DB 23;
Pred. No. 5.63e-03;
49; Mismatches 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (24-JUL-1998) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
On Jul 24, 1998 this sequence version replaced gi:3241936.
Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA e-mail address: humgen@tigr.org. The orientation of the sequence is from SP6 end to T7 end. Genes were identified by a combination of five methods including: xGRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, Washington), Genscan (Chris Burge, Washington)
                                                                                                                                                                                                                                                                                                                                                                                                                            http://gnomic.stanford.Edu/-chris/GENSCANW.html)searches of the complete sequence against a peptide database, and the Human gene Index database at TIGR (http://www.tigr.org/tdb/hgi/hgl.html).
Genes without pepetide homolgy having spliced EST hits are termed 'Unknown gene product'. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bjloftus@tigr.org
3 (bases 1 to 216021)
Adams,M.D. and Loftus,B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-JUN-1998) The Institute for Genomic Research, medical Center Dr. Rockville, MD 20850, USA, Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 216021)
Adams,M.D. and Loftus,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams,M.D., Loftus,B.J., Zhou,L., Crosby,M., Fuhrmann,J., Mason,T.M., Brandon,R., Kim,U.J., Kerlavage,A.R. and Venter,J.C. Homo sapiens Chromosome 16 BAC clone CIT9875K-A-952F10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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Homo sapiens Chromosome
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27765. .27872
/note="9824, WI-3555, Chr. 16, Homo sapiens"
/db_xref="dbsT5:004388"
51778 c 49172 a 53007 -
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/note="16084, CHLC.GCT10802, Chr.
/db_xref="dbSTS:G09703"
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                                                                                                                                                                              sapiens"
/db_xref="dbSTS:G02122"
                                                                                                                                                                                                                                                                    sapiens"
                                                       /note="16316, CHLC.GCT15C04, Chr.
/db_xref="dbSTS:G09935"
199463. .199572
                                                                                                                                                                                                                /note="7608, STS1-cSRL-24g1-uA/cSRL-24g1-uZ,
                                                                                                                                                                                                                                                                                                                                     /map="#16q21-22"
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/chromosome="16"
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                                                                                                                                                                                                                                                   xref="dbSTS:G02280"
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16 BAC clone CIT987SK-A-952F10, complete
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128278.1
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AR024229
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Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H. Plant inhibitors of fungal polygalacturonases and control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
                                                                                          Kitamura, K.

Recombinant human anti-Lewis b antibodies
Patent: US 5795961-A 22 18-AUG-1998;
                                                                                                                                         1 (bases 1 to 965)
Wallace, T. Paul, Harris, W.J., Carr, F.J., Old, L.J., Welt, S. and
                                                                                                                                                                                                                                                     g3977523
AR024229.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.3%;
Similarity 20.0%;
22; Conserva+***
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                        /organism-"unknown"
170 c 226 g
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8 c 25 g
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42; Mismat
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1. No. 2.17e-02;
Mismatches 45;
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Best Local Similarity 34.1%;
Matches 30; Conservative
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CC strandedness
CC topology: Li
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AC003030
                     Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 60966)
                                                                                                                                           HTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent: JP
TEIJIN LTD
OS Hepati
PN JP 199
PD 04-DEC
PF 29-MAY
PI MORINA
                                                                                         Homo sapiens
                                                                                                                                                                                                                                                 Homo sapiens chromosome
                                                                                                                                                               AC003030.1
                                                                                                                                                                                                                                                                           AC003030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C-like viruses.

1 (bases 1 to 565)

MOIInaga, T., Chayama, K., Kumada, H. and Ichikawa, Y..

NUCLEIC ACID FRACMENT WITHIN ENVELOPE REGION OF HEPATITIS C VIRUS
AND METHOD FOR DETECTING THE SAME
PATENT: JP 1992349885-A 1 04-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g2172286
E04076.1 GI:2172286
JP 1992349885-A/1.
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Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus
JF 199349885-A/1
04-DEC-1992
29-MAY-1991 JF 1991152169
MORINGA TSUTAE, CHAYAMA KAZUAKI, KUMADA HIROMITSU, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C12N15/10,C12Q1/68,C12Q1/70//C12N15/11; strandedness: Single;
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                                                                                                                                                                                                                           sequence.
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/db_xref="taxon:11103"
93 C 107 g 85 t
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                                                                                                                                                            GI:4092821
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Pred. No. 3.
29; Mismatc
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Pred. No. 8.16e-02;
41; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 g
                                                                                                                                                                                                                                              DNA
19,
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                                                                                                                                                                                                                                            overlapping cosmids R29828 and F25496,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.00e-01;
+ches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 565;
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Map and sequence oriented from ptelomere to centromere. This accession is comprised of overlapping cosmids R29828 (bases 1 to 40,974) and F25496 (bases 23,336 to 60,966). R29828 is separated from cosmid F23586 (AC004475) to the left by a Sequence gap of approximately 14 kb, which is to be filled by sequencing a restriction fragment from cosmid R27336 (currently in progress). Cosmid R25496 is separated from cosmid R37336 (currently in progress). Cosmid R25496 is separated from cosmid R37363 to the right by an expected sequence gap of at least 10 kb. Additional chr 19 map and betweence information are available at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lamerdin, J.E., McCready, P.M., Skowronski, E., Viswanathan, V., Burkhart-Schultz, K., Gordon, L., Dias, J., Ramirez, M., Stilwagen, S., Phan, H., Velasco, N., Do, L., Regala, W., Terry, A., Garnes, J., Danganan, L., Erler, A., Christensen, M., Georgescu, A., Avila, J., Liu, S., Attix, C., Andreise, T., Trankheim, M., Amico-Keller, G., Coefield, J., Duarte, S., Lucas, S., Bruce, R., Thomas, P., Quan, G., Krommiller, B., Arellano, A., Sanders, C., Ow, D., Nolan, M., Trong, S., Kobayashi, A., Olsen, A.S. and Carrano, A.V. Sequence analysis of a 2 Mb contig in 19p12 between UBAS2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (04-JAN-1999) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (28-OCT-1997) Human Genome Center, Joint Institute/ Lawrence Livermore National Laboratory, Livermore, CA 94551, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www-bio.llnl.gov/genome/genome.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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4 (bases 1 to 60966)
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/note-"DDS similarity to overlapping ESTs:-AA963316
UT-R-E1-gi-c-06-0-UI.s1 UI-R-E1 Rattus norvegicus cDNA
clone UI-R-E1-gi--06-0-UI 3', (220. .237); 100%
identity.--AA893275 EST197078 Normalized rat kidney, Bento
Soares Rattus sp. cDNA clone RKIBE38 3' end; (240. .257);
                                                                                                                        /rpt_family="AluJo" 5028. .5045
                                                                                                                                                                                                                                                   complement(1148. .1315)
/note="predicted exon, program: grail2exons_human_1.3,
frame: 2, quality: good, score: 51.000"
complement(1477. .1706)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /map="19p12 between UBA52 and D19S455."
/Cell_line="UV9HL9-5B for F25496, and 5HL2-B for R29828"
/clone_lib="FL19NC02 (for F25496) and L119NC03 (for R29828) chromosome 19-specific cosmid libraries"
/note="Cosmid libraries constructed at LLML from flow-sorted chromosomes from human-hamster hybrid cell lines UV5HL9-5B and 5HL2-B, each of which carries chromosome 19 as its only human chromosome."
                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="Aluy"
930. .1066
                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="AluJo"
530. .824
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/chromosome="19"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                  rpt_family="AluJo"
                                                                                                                                                                                       _family="AluSp"
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//db_xref="pid:94105883"
//db_xref="gid:94105883"
//db_xref="gid:94105883"
//db_xref="gi:4106983"
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//translation="wiscoipepedvkfeaasilselycoensydaakpilskchil
sootpywhchlfolopipepedvkacdllgycoapyapvgsgytralfeliskchil
sootpywhchlfilecoipepedkerpelverplucytrythyndagoyksykepe
lkkoloociotistihddellpspkpadlehhepkehkovlyvlythyndagoyksykepe
lkkoloociotistihddellpspadlehepkehkovlyvlythyndagoyksykepe
kytdkalmolekikhildcspilssfovillehiimcrlytghkatalgeglycysvo
kytdkalmolekikhildcspilssfovillehiimcrlytghkatalgeglycysvo
kytdkalmolekikhildcspilssfovishelanafyyrglisffogrysvol
kytdkalmolekitasilehiindhsforsshelmiltspichiimcrlythychweg
lantrepanolaheaaomhonfsoollodhieacslpehnlityrvghweg
iaatrepanolaheaaomhonfsoollodhieacslpehnlityrvghweg
iaatrepanolaheaaomhonfsoollod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   frame: 0, quality: excellent, score: 94.000--DDS similarity to overlapping ESTs: (8155 . 8237) A8963316 UT-R-E1-g1-C-06-0-UT-S-1 UT-R-E1 Rattus norvegicus cDNA clone UT-R-E1-g1-C-06-0-UT-3; (400. .482); 88% identity. --8155 . 8240) A883275 EST197078 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone RKIBE38 3' end; (420. .485); 85% identity.
                                                                                                                                                                                                                                                                                                                                                                                       complement(8872. .8996)
/rpt_family="Aludb"
9052. .9196
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(A80. .6575

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(A80. .6576

(A80.
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/rpt_family="AluJo"
6480..6575
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                                                                                                                                                                                                                                                    /rpt_family="Alux" 9494. .9658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="AluJb"
8480. .8768
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8155. .8249
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/product="R29828_1"
                                                                                                                                                                                                                                                                                                                               /rpt_family="Alusx" 9197. .9493
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/note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: excellent, score: 86.000"
10562. .10721
                                                                                                                                                                             /rpt_family-"Alusx"
9668 .9967
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                                                                                                          /rpt_family="AluY"
10156. .10183
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AUTHORS
TITLE
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KEYWORDS
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                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.5%;
Best Local Similarity 85.7%;
Matches 30; Conservative
                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
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A62989
93716861
A62989.1 G
                                                                                                                                          1 (bases 1 to 60)

OFHUM, H. and Seeger, C.

METHOD FOR GENERATING MULTIPLE DOUBLE STRANDED NUCLEIC ACIDS PATENT: WO 9720068-A 1 05-JUN-1997;

BOEHRINGER MANNEIM GMBH (DE)
                                                                                                                                                                                                                                                                                                                                                                           unidentified
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frame: 1, quality: excellent, score: 100.000"
11845. .11991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="AluY"
20234. .20341
/rpt_family="AluJo/FLAM"
complement(20344. .20655)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"predicted exon, program: grail2exons_human_1.3, frame: 0, quality: excellent, score: 89.000"
18465. .18542
/note-"predicted exon, program: grail2exons_human_1.3, frame: 0.744
1858: 10744
1858: 10744
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/note="DDS similarity to AA212842 mw82d12:r1 Soares mouse

/not = "DDS similarity to AA212842 mw82d12:r1 Soares mouse

NML Mus musculus cDNA clone 677207 5'; (200. .468); 80%
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frame: 2, quality: excellent, score: 97.000"
complement(19286. .19309)
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frame: 0, quality: excellent, score: 97.000"
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19929. .20226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="AluSx"
19632. .19928
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frame: 0, quality: excellent, score: 100.000"
16463. .16747
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frame: 2, quality: excellent, score: 100.000"
13440. .13741
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frame: 1, quality: excellent, score: 96.000"
           /organism="unidentified"
/db_xref="taxon:32644"
                                                                                                                  Location/Oualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:3716861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _family="POLY_A"
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n Patent
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Pred. No. 3.00e-01;
0; Mismatches 5
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KEYWORDS
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Best Local Similarity 10.8%;
Matches 7; Conservative
                       AUTHORS
                                                                       JOURNAL
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Best Local Similarity 6.2%;
Matches 2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             670 MVRGK 674
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                                                                                Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Gatarrhini; Hominidae; Homo.

1 (bases 1 to 175793)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone hRPK.700_H_6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Direct Submission
Submitted (27-JAN-1997) Breeding and Genetics, Danish Institute of Submitted (27-JAN-1997) Breeding and Genetics, Danish Institute of Animal Science, Blichersalle K25, Tjele 8830, DK
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome AC005920
  2 (bases 1 to 175793)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.

1 (bases 1 to 1056)
Brusgaard,K., Shukri,N.M., Malchenko,S., Koroleva,I. and Lohi,O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U87256
g4099442
U87256.1 GI:4099442
                                                                    Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /standard_name="1167F"
complement(300. .320)
/standard_name="1167R"
221 c 210 g 2
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/map="1g"
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/db_xref="taxon:9667"
                                                                                                                                                                                                                                                                                                                                                                                                                          175793 bp
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GT dinucleotide repeat, chromosome 1q.
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Pred. No. 1.07e+00;
40; Mismatches 17;
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Pred. No. 1.07e+00;
26; Mismatches 4
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17, clone hRPK.700_H_6, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 others
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Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C., Barcwin, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Corliss, D., Depayre, E., Devon, K., Dewar, K., Donelan, L., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Geralgery, K., Grant, G., Hagos, B., Heaford, A., Herena, L., Horton, L., Howland, J.C., Jacotot, L., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrin, J., Molla, M., Morris, W., Morrow, J., Mychalecky, J., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Stope, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella, Miller, I., Ve, M., Wo, H., Wo, M., Wagner, A., Wheeler, J., Wu, Y., Wyman, D., Ye, W., Tand, T., And T., And T., Tand, T., Tand,
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Direct Submission
Submitted (25-NOV-1998) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Nov 25, 1998 this sequence version replaced gi:3924659.

All repeats were identified using RepeatMasker: Smit, A.F.A. &
Green, P. (1996-1997)
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Note: remainder of annotations omitted.

Db 18898 GGTGG 18902 |||||| Cp 7 GGTGG 3 Сþ Query Match 10.1%; Best Local Similarity 72.3%; Matches 47; Conservative 67 GGCAGCCCAGACCCCATAGTGGCCACTGCGCTCCTGGGATGGAGGAGACACTGAAGTCCC 8 Score 24; DB 31; Length 175793; Pred. No. 1.07e+00; 0; Mismatches 17; Indels 1: Gaps 1;

Search completed: Sun Oct 24 16:30:24 1999 Job time: 485 secs.

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claim 4; Page 135, 178pp; End Claim 4; Page 135, 178pp; End This is the nucleotide sequent includes a coding region (ali- transmembrane protein (see My stomach cancer cDNA library of method, and by protein synth encoded protein has a putati- internal transmembrane domain internal transmembrane domain	730/04. 730/04. 498. roteins containinguences useful	98. 98; J02445. 97; JP-144948. ROTEGENE INC. AGAMI CHEM RES CENT. AGAMI CHEM RES CENT.		· e h	8.8 5003 51	8.8 911 52 8.8 911 51	8.8 908 51 8.8 908 52 8.8 908 52	9.2 82 21 9.2 89 32 9.2 91 46 9.2 190 32 9.2 264 32 9.2 368 35	9.7 114 12 9.7 114 12 9.7 565 6 9.2 36 2 9.2 375 21 9.2 75 21 9.2 81 21	10.5 114 12 10.1 114 12 10.1 114 12 10.1 114 12 10.1 114 12 10.1 114 12 10.1 114 12	12.6 114 12 12.2 114 12 12.2 114 12 12.2 114 12 11.8 114 12 11.8 178 32 11.3 172 32 10.9 114 12 10.9 114 12
claim 4; Page 135; 178pp; English. This is the nucleotide sequence of cDN includes a coding region (also claimed transmembrane protein (see N88498). T stomach cancer cDNA library using a si method, and by protein synthesis by in encoded protein has a putative signal internal transmembrane domain. The in sequences (see V88359-76) coding for 1	730/04. 498. roteins containing transmen	II GEN		· e h	8.8 5003 51	8.8 911 52 8.8 911 51	8.8 908 51 8.8 908 52 8.8 908 52	9.2 82 21 9.2 89 32 9.2 91 46 9.2 190 32 9.2 264 32 9.2 368 35	9.7 114 12 9.7 114 12 9.7 565 6 9.2 36 2 9.2 375 21 9.2 75 21 9.2 81 21	10.5 114 12 10.1 114 12 10.1 114 12 10.1 114 12 10.1 114 12 10.1 114 12 10.1 114 12	12.6 114 12.2 114 12.2 114 12.2 114 11.8 114 11.8 114 11.3 117 11.3 172 10.9 114 10.9 30
each production, gene diagnosis, 5, 178pp: English. sortide sequence of cDNA clone if gregion (also claimed) for a rotein (see w88498). The clone DNA library using a signal sequence in synthesis by in vitro thas a putative signal sequence abrane domain. The invention if 84359-76) coding for 18 transme	730/04. 730/04. 498. quences - useful in the preparation	98. 99; JD2445. 97; JF-144948. ROTEGENE INC. AGAMI CHEM RES CENTRE.	Location/Qualifiers 75.311 /*tag= a /note= "cDNA comprising the stop codon)	ALIGNMENTS (ard; cDNA to mRNA; 439 BP. (first entry) (h carcinoma cDNA clone HP1(p protein; HP10408; human;	8.8 5503 51 V63020	8.8 911 52 V63312 Nuc 8.8 911 51 V63012 D.	8.8 908 51 V63024 8.8 909 52 V63315 8.8 908 51 V63024 8.8 909 51 V63024	9.2 82 21 T13610 9.2 89 32 T76219 9.2 91 46 V44650 9.2 190 32 T76452 9.2 264 32 T76445 9.2 3088 16 T05628 9.8 168 27 T56528	9.7 114 12 070471 9.7 114 12 070471 9.7 565 6 035072 9.2 36 2 011195 9.2 75 21 T13612 9.2 81 21 T13611	10.5 114 12 Q70473 10.5 250 32 T76438 10.1 114 12 Q70473 10.1 114 12 Q70466 10.1 114 12 Q70466	12.6 114 12 070468 12.2 114 12 070465 12.2 114 12 070465 12.2 114 12 070469 11.8 114 12 070465 11.8 178 32 776405 11.3 114 12 070466 11.3 172 32 776363 10.9 114 12 070472 10.5 30 7 064787
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case PUBLES production, gene diagnosis, and gene therapy; Page 135; 178pp; English. the nucleotide sequence of cDNA clone HP10408, which s a coding region (also claimed) for a novel human mbrane protein (see M88498). The clone was isolated from a cancer cDNA library using a signal sequence detection and by protein synthesis by in vitro translation. The protein has a putative signal sequence and a putative litransmembrane domain. The invention provides nucleotide transmembrane domain. The invention provides nucleotide s (see V84359-76) coding for 18 transmembrane proteins	WPI, 99-045730/04. P-PSDB; W88498. New human proteins containing transmembrane domains and their encoding sequences - useful in the preparation of antibodies and	98. 99; JD-144948. 97; JF-144948. ROGANI CHEM RES CENTRE.	Location/Qualifiers 75.311 /*tag= a /note= "cDNA comprising the coding region (the stop codon) is claimed (Claim)	ALIGNMENTS (ard; cDNA to mRNA; 439 BP. (first entry) (h carcinoma cDNA clone HP1(p protein; HP10408; human;	8.8 509 51 V63020 D. immitis ankyrin nD	8.8 911 52 V63312 Nucleotide nDiAnk911 8.8 911 51 V63012 D. immitis ankyrin nD	8.8 908 51 V63025 B. malayi ankyrin cDN 8.8 908 52 V63315 Nucleotide nBmAnk908 8.8 908 51 V63024 B. malayi ankyrin nBm 8.8 908 51 V63024 B. malayi ankyrin nBm	9.2 82 21 T13610 DC43 TSAR library gen 9.2 89 32 T76219 Human IL5 antisense o 9.2 91 46 V44650 Mammalian DNA replica 9.2 190 32 T76452 Chymase antisense oli 9.2 264 32 T76445 Substance P receptor 9.2 3088 16 T05628 ADP ribosylation fact	9.7 114 12 070471 Generic DNA sequence 9.7 114 12 070471 Generic DNA sequence 9.7 565 6 035072 HCV envelope region n 9.2 36 2 011195 Ballast Constituent c 9.2 75 21 T13612 DC43 TSAR Library gen 9.2 81 21 T13611 DC43 TSAR Library gen	10.5 114 12 Q70473 Generic DNA sequence 10.1 114 12 Q70473 Generic DNA sequence 10.1 114 12 Q70473 Generic DNA sequence 10.1 114 12 Q70466 Generic DNA sequence 10.1 114 12 Q70473 Generic DNA sequence 10.1 114 12 Q70473 Generic DNA sequence	12.6 114 12 070468 12.2 114 12 070465 12.2 114 12 070465 12.2 114 12 070469 11.8 114 12 070465 11.8 178 32 776405 11.3 114 12 070466 11.3 172 32 776363 10.9 114 12 070472 10.5 30 7 064787

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                                                                                                                                                                                                                                                        samples Claim 3: Page 14; 23pp; English.
Consists of nucleotides 5-95 of (051735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also 051735-45 and 051747-59.
Secuence 91 BP; 5 A; 17 C; 15 G; 4 T;
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EP-571911-A.
01-DEC-1993.
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New Oligo:nucleotide probes specific for Mycobacteria - detection and amplification of Mycobacteria nucleic acid
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Q51746 standard;
08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutic Escherichia coli.
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26-MAY-1992; US-889651
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Oligonucleotide; DNA probe; r
                                                              N81164 standard;
N81164;
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llarity 99.2%;
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Pred. No. 1.08e-132;
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NN EP-285123-A.

10 05-MAY-1988: 105163.

10 03-MAR-1988: 105163.

11 Cahtovasara P. Knowles J. Koivula A. Bamford J. Reinikainen T;

12 Lahtovasara P. Knowles J. Koivula A. Bamford J. Reinikainen T;

13 WPI: 88-279927/40.

14 WPI: 88-279927/40.

15 Introducing random point mutations into nucleic acods -

17 Introducing random point mutations into nucleic acods -

18 WPI: 88-279927/40.

19 by prepn of single stranded template, annealing a primer, elongation by prepn of single stranded template of molecules and screening.

10 Introducing random point mutations were introduced into the alpha fragment of Random point mutations were introduced into the alpha fragment of E. coli beta-galactosidase. The wild type sequence was obtained as E. coli beta-galactosidase. The wild type sequence was obtained as E. coli beta-galactosidase. The wild type sequence was obtained as Single stranded template and an oligonucleotide was bybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The
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30-MAR-1988; 10
03-APR-1987; US
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Introducing random point mutations into nucleic by prepn of single stranded template, annealing misincorporation, completion of molecules and so Disclosure; p; English.
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Base substituted E.coli beta-galactosidase alpha-fragment.
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US-034819.
EN SOKERI OY.
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No. 3.39e-08
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Q70470 standard; 1
Q70470;
10-APR-1995 (fir
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EP-571911-A.
01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
                WO9418318-A.
18-AUG-1994,
01-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 14; 23pp; English.

Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (051735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also 051735-45 and 051747-59.

Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                        Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding de effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which occurred singularly in any given mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q51746
Q51746;
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Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; n
                                                                                                                             misc_feature
                                                                                                                                                                         Synthetic.
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54; Misma
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has 7;
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Identifying proteins or peptide(s) which bind a ligand - screening a recombinant vector library expressing fusion comprising a binding domain and an effector domain
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                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
Key
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Identifying proteins or peptide(s) which bind a ligand - by
PT screening a recombinant vector library expressing fusion proteins
promprising a binding domain and an effector domain
PS Disclosure; Page 35; 255pp; English.

CC 070470 is a generic DNA sequence used to generate random TSAR (Totally
CC Synthetic Affinity Reagents) peptides. This generic formula can also be
CC represented as follows: X(NNB)4(CAC)(NNB)4(CAC)(NNB)82(NNB)5(CAC)(NNB)8

C -(CAC)2(NNB)x. x and y are flanking restriction sites (X is not the same
CC as Y) that are not specified further. The peptides generated by this and
CC other generic sequences (070471-73) have invariant histidine residues
C1 incorporated into variant sequences. TSARs are concatenated
CC tergions - a binding domain with affinity for a ligand and a second
CC regions - a binding domain with affinity for a ligand and a second
CC deffector peptide portion that is chemically or biologically active. They
CC may further comprise a linker peptide between the 2 domains. The TSARs
CC deliver a chemically or biologically active moiety, eg. metal ion,
CC radioisotope, peptide toxin or enzyme, to the specific target or on the
CC cell. They can also replace the function of macromolecules, eg.
CC complex methods of hybridoma formation or in vivo antibod.
W09418318-A.
18-AUG-1994; U00977.
01-FEB-1994; U5-013415.
01-FEB-1993; U5-013415.
30-DEC-1993; U5-176500.
31-JAN-1994; U5-189331.
(UYNC-) UNIV NORTH CAROL
FOWLKS- DM, KAY BK;
WPI; 94-779739/34.
P-PSUB; R65153.
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30.DEC-1993; US-776500.
31.JAN.1994; US-189331.
(UYNC-) UNIV NORTH CAROL
FOWLKES DM. KAY BK;
WPI; 94-279739/34.
P-PSDB; R58378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding dom: effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
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les 7; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGGTCTGGGCTGCCCCTTGTCCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/note= "this sequence represents 'Z'; Z
sequence of 5, 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 55..60
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                                                                                                                                            CAROLINA
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Pred. 1
28; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 12;
6.14e-05;
6.8;
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PS Disclosure; Page 35; 255pp; English.

CC 0770467 is a generic DNA sequence used to generate random TSAR (Totally CC Synthetic Affinity Respents) peptides. This generic formula can also be CC represented as follows: X(NNB)16(TGC)(NNB)12(NNB)15(TGC)(NNB)17. X CC and Y are flanking restriction sites (X is not the same as Y) that are CC and Y are flanking restriction sites (X is not the same as Y) that are CC controlled further. Other generic sequences are shown in 070466-68.

CC Other specific peptides generated by these generic sequences are shown in CC comprising at least two functional regions - a binding domain with call of the sequences are shown in the comprising at least two functional regions - a binding domain with call the sequences are shown in CC cohemically or biologically active. They may further comprise a linker cc peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned CC in or flanking, the unpredicted or variant residues. These residues CC confers some degree of conformational rigidity to the peptides. The TSARs CC compsns. comprising a TSAR binding domain can be used in vivo to CC deliver a chemically or biologically active molety, eg. metal ion, cc. compsns. comprising a TSAR binding domain can be used in vivo to CC monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. CC mentional can be detection in a screening process.

Squence 114 BP; 0 A; 2 C; 2 G; 2 T;
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Best Local
                                                                                                                                                                                                                                                                                                 W09418318-A.
18-AUG-1994; U00977.
01-FEB-1994; U5-013416.
30-DEC-1993; US-176500.
31-DAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWLKES DM, Kay BK;
WPI; 94-779739/34.
P-PSDB: R65154.

Identifying proteins or peptide(s) which bind a ligand by Identifying proteins or peptide(s) which bind a ligand by Identifying proteins or peptides in the proteins screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain pisclosure; Page 35; 255pp; English.

Q70468 is a generic DNA sequence used to generate random TSAR (Totally Q70468 is a generic DNA sequence used to generate formula can also be represented as follows: X(NNB)11(TGC)(NNB)63(NNB)7(TGC)(NNB)10Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68.

Other specific peptides generated by these generic sequences are shown in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding defector domain; concateneated heterofunctional protein; link direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /uoce= "this sequence represents 'Z', Z sequence of 6, 9 or 12 nucleotides (see comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 55..60
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Pred. No.
30; Misma
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, 6.14e-05;
.--ches 74;
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                                                                                                                                                                                                            CC comprising at least two functional regions - a binding domain with CC affinity for a ligand and a second effector peptide portion that is CC chemically or biologically active. They may further comprise a linker CC peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned CC in, or flanking, the unpredicted or variant residues. These residues CC confer some degree of conformational rigidity to the peptides. The TSARs CC crompsns. comprising a TSAR binding domain can be used in vivo to CC deliver a chemically or biologically active molety, eg. metal ion, CC cradicisotope, peptide, toxin or enzyme, to the specific target or on the CC cell. They can also replace the function of macromolecules, eg. CC monocional or polyclonal antibodies and therefore circumvent the need CC complex methods of hybridoma formation or in vivo antibody CC groduction. The TSARs are easily characterised and have designed activity SQ Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
                                                                                                                                 Matches
                                                                                                                                                   Query Match
Best Local
  69
                                            19
                                                                                                                                                   Local Similarity
                                                                                    9
                                          GTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCC
bnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbnnbnnb
                                                                                    bnnbnnbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnnnnnnnnbnnbnn
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                                                                                                                                 Conservative
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                                                                                                                              Score 30;
Pred. No.
30; Misma
                                                                                                                                   Mismatches
                                                                                                                                                        2.07e-04;
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DR P-PSDE R88378.

DR P-PSDE R88378.

PT Identifying proteins or peptide(s) which bind a ligand - by PT Identifying proteins or peptide(s) which bind a ligand - by PT screening a recombinant vector library expressing fusion proteins pT comprising a binding domain and an effector domain PT Disclosure; Page 36; 255pp; English.

CC 070470 is a generic DNA sequence used to generate random TSAR (Totally CC officially Reagents) peptides. This generic formula can also be CC represented as follows: X(NNB)4(CAC)(NNB)4(CAC)(NNB)8(X(NNB)6(CAC)(NNB)8 (CAC)(NNB)8 (CAC) (NNB)8 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-AUG-1994; UO1-FEB-1994; UO1-FEB-1993; UO1
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Q70470;
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US-176500.
US-189331.
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Сþ В Сþ Ъ

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RESULT

AC 077

AC 077
                                           In Identifying proteins or peptide(s) which bind a ligand - by PT Screening a recombinant vector library expressing fusion proteins processing a recombinant vector library expressing fusion proteins processing a binding domain and an effector domain processing a binding domain and an effector domain proteins processing a binding domain and an effector domain proteins or peptides; page 33; 255pp; English.

CC 070468 is a generic DNA sequence used to generate random TSAR (Totally CC Synthetic Affinity Reagents) peptides this generic formula can also be CC represented as follows: X(NNB)11/TGC)(NNB)52(NB)1/TGC)(NB)10/Y. X (CC and year flanking restriction sites (X is not the same as Y) that are CC contributed further. Other generic sequences are shown in 070466-68.

CC affinity for a ligand and a second effector peptide portion that is comprising at least two functional regions - a binding domain with a finity for a ligand and a second effector peptide portion that is comprising at least two functional regions - a binding domain with heavy research peptide contains 2 or 4 cysteine residues positioned CC in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs comprising a TSAR binding domain can be used in vivo to CC deliver a chemically or biologically active moiety, eg. metal ion, call of the peptides of the TSARs are easily characterised and have designed activity sequence 114 Bp; 0 A; 2 C; 2 G; 2 T;
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01-FEB-1993; US-011416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV WORTH CAROLI FOWLKES DM, KAY BK;
WPI; 94-279739/34.
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Matches Query Match Best Local

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PT Identifying proteins or peptide(s) which bind a ligand - by Identifying proteins are peptide(s) which bind a ligand - by Identifying proteins are peptides of the comprising a binding domain and an effector domain proteins processing a binding domain and an effector domain proteins proteins proteins are comprising a binding domain and an effector domain proteins proteins proteins are shown in proteins of the same as proteins are shown in construction sites (X is not the same as Y) that are conditional regions - a binding that are conditional regions - a binding that are comprising at least two functional regions - a binding domain with comprising at least two functional regions - a binding domain with comprising at least two functional regions - a binding domain with comprising at least two functional regions - a binding domain with comprising at least two functional regions - a binding or peptides. Comprising at least two functional regions - a binding or peptides. Comprising at least two functional regions - a binding or peptides. Comprising at least two functional regions - a binding or peptides. Comprising at least two functional regions - a binding or peptides or that is comprised peptide contains 2 or 4 cysteine residues positioned conformational regions are also designed so conformational rigidity to the peptides. The TSARS correspondence are comprised, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. metal ion, or flanking, the unpredicted or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. metal conformational rigidity to the specific target or on the cell. They can also replace the function of macromolecules, eg. conformational repolace and therefore circumvent the need conformation of macromolecules and the conformation of recomplex metals and the conformation of the conformation o
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30-DEC-1993; US-176500.
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(UYNC-) UNIV NORTH CARCLINA.
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                                                                                                                                                                                                                                                                                                                                                                                                      Score 29;
Pred. No. 6
29; Mismat
                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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matches 66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 114;
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PT identifying proteins or peptide(s) which bind a ligand - by PT identifying proteins or peptide(s) which bind a ligand - by PT screening a recombinant vector library expressing fusion proteins PT comprising a binding domain and an effector domain
PS Disclosure; Page 35; 25pp; English.
CC 970469 is a generic DNA sequence used to generate random TSAR peptide
CC 970469 is a generic DNA sequence used to generate random TSAR peptide
CC 970469 is a generic DNA sequence used as follows: XIGC)(NNB)10-CC
CT fils generic sequences (NNB)14/GCC)Y. X and Y are flanking restriction
CC sites (X is not the same as Y) that are not specified further. This
CC sequence generates peptides that are cloverleaf in Structure. Other
CC generated by these generic sequences are shown in R65150-54. TSARs are
CC concatenated heterofunctional proteins or peptides, comprising at least
CC a second effector peptide portion that is chemically or biologically
CC a second effector peptide portion that is chemically or biologically
CC active. They may further comprise a linker peptide between the 2 domains.
CC contains 2 or 4 cysteine residues positioned in, or flanking, the
CC contains 2 or 4 cysteine residues positioned in, or flanking, the
CC contains 2 or 4 cysteine residues positioned in, or flanking, the
CC contains 2 or 4 cysteine residues. These residues confer some degree of
CC contains 2 or to the specific target or on the cell. They can also replace
CC contains of macromolecules, eg. mencal ion, radioisotope, peptide, toxin
CC and therefore circumvent the need for complex methods of hybridoma
CC contains of macromolecules, eg. mencal contended in hybridoma
CC contains of a screening process.
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SXXXX
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Best Local
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01-FEB-1994; U00977.
01-FEB-1993; US-013416.
01-FEB-1993; US-176500.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOW1kes DM, KAY BK;
WPI; 94-279739/34.
          IT 14
(70465;
Q70465;
Q70465;
O5-APR-1995 (first entry)
O5-APR-1995 (first entry)
OF-APR-1995 (forst entry)
TSAR; totally synthetic affinity reagent; synthetic; binding of
TSAR; totally synthetic affinity reagent; synthetic; binding of
effector domain; concateneated heterofunctional protein; linke
olirect; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      girect; rapid;
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Generic DNA sequence to generate a random TSAR peptide library TSAR; totally synthetic affinity reagent; synthetic; binding dereffector domain; concateneated heterofunctional protein; linker direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q70469;
07-APR-1995
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                                                                                                                                                                                                            CGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGC
                                                                                                                                                                                                                                                                                                                           cnnbnnbnnbnnbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnnnnnnn
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114 BP; 0 A;
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                                                                                                                                                                                                                                                                                                                                                                   Conservative
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/note= "this sequence represents '2'; Z can
sequence of 6,9 or 12 nucleotides (see
comments)"
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                                                                                                                                                                                                                                                                                                                                                                                      12.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              process.
A; 4 C;
                                                                                                                                                                                                                                                                                                                                                               Score 29;
Pred. No.
29; Misma
                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                4 G;
                                                                                                                                                                                                                                                                                                                                                                                        6.89e-04;
                                                                                                                                                                                                                                                                                                                                                                                                        DB 12;
                                                                                                                                                                                                                                                                                                                                                                     75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                4 T;
                                                                                                                                                                                                                                                                                                                                                                                                        Length 114;
                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                            domain;
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                              66
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RESULT TO DT 11 DT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ç
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Best Local Similarity 3.6%;
Matches 4; Conservative
                                                                 Synthetic.

W09640162-A1.

19-DEC 1996.
06-JUN-1996. U09306.
07-JUN-1995. US-474497.
(UVEC-) UNIV EAST CAROLINA.
Metager WJ, Nyce JW;
WPI: 97-051871/05.
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18-AUG-1994; U00977.

01-FEB-1994; US-013416.

30-DEC-1993; US-175500.

31-ANN-1994; US-189331.

(UYNC-) UNIV NORTH CAROLINA.
FOWLKES DM, Kay BK;
WPI: 94-279739/34.

P-950B; R65150 and R65151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human endothelin-1 antisense oligonucleotide.
Asthma; airway epithelium; adenosine free; cystic fibrosis; chronic obstructive pulmonary disease; bronchitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T76405 standard; DNA; 178 BP T76405;
Treatment of airway diseases such as asthma - by topically applying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 TCAGCTTCAGTTGCAAAGTCATACCCGGCCCTGTTCCATGTGAGCTGCCAAGGAGGGTCA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 AGAGGAGACAAGGGGCAGCCCAGACCCCATAGTGGCCACTGCGCTCCTGGG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 bnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbtgcnnbnnbnnb 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 խոսխողխողխողխութեցշողխողխողխողխողխողխողխողխողխողխողողորոր 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note* "this sequence represents '2'; Z can sequence of 6, 9 or 12 nucleotides (see comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 55..60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28; DB 12; Length 114;
Pred. No. 2.27e-03;
30; Mismatches 78; Indels
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PT subject
PS claim 5; Page 38; 71pp; English.
CC A method for treating airway disease in a subject has been produced,
CC which involves the topical administration of an essentially adenosine
CC free antisense oligonucleotide (ON) to the airway epithelium of the
CC subject. The present sequence is an antisense oligonucleotide specific
CC for the human endothelin-1, targeted at the initiation codon. The
CC method can be used to treat airway disease such as cystic fibrosis,
CC asthma, chronic obstructive pulnoary disease, bronchitis and other
CC airway disease characterised by an inflammatory response. By
CC eliminating adenosine from the antisense ON, its liberation upon
CC antisense degradation is prevented, thereby preventing adenosine-
CC induced bronchoconstriction in patients with hyper-reactive airways.
Sequence 178 BP; 0 A; 52 C; 46 G; 32 T;
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                                                     В
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                                                                                                                                                                                                                                                                                        Query Match 11.8%;
Best Local Similarity 32.0%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adenosine-free antisense oligo:nucleotide to airway epithelium
                                        129 btcbtgbgcbbbtbbtccbttctgbbbbbbbbgggbtcbbb 168
61 GCCTGCCCTTGTCCTCCTCTTGACCCTCCTTGGCAGCTC 100
                                                                                                                  71 bgcgcctbbgbctgctgtttcttggbgc-tccttggcbbgccbcbbbc-bgcbgbgbbbb 128
                                                                                      1 GCCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTG 60
                                                                                                                                                                                  Score 28; DB 32; L4
Pred. No. 2.27e-03;
37; Mismatches 29;
                                                                                                                                                                                                                                Length 178;
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Search completed: Sun Oct 24 16:40:11 1999
Job time: 78 secs.

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			Sequence 32,																						Sequence 41
	Applicatio		Applicati														Applicati		Agg	Appl	Appl	App1	Appl	Appl	
	1.89e+00		5.69e-01	.69e-	.69e-	. 69	. 69e					5.69e-01		.69e-	5.69e-01	. 69e-	5.69e-01	. 69e-		5.69e-01					5.69e-01

ALIGNMENTS

Sequence 14, Application US/08232463
Septicanii Dorner, F.

C APPLICANI: DORNER, F. G.
APPLICANI: PALKNER, F. G.
APPLICANI: PALKNER, F. G.
APPLICANI: POPPY OF A CONFORMER PROBLEM FORM:
C COMPUTER: USA
C COMPUTER: IBM PC COMPATIBLE OF APPLICATION UNMBER: US/08/232,463
C COMPUTER: PATENTIA Release #1.0, Version #1.25
CURENT APPLICATION UNMBER: US/08/232,463
C CURENT APPLICATION NUMBER: US/08/232,463
C CLASSIFICATION NUMBER: US/07/935,313
FILING DATE:
C APPLICATION NUMBER: US/07/935,313
FILING DATE:
C APPLICATION NUMBER: EP 91 114 300.6
FILING DATE:
C APPLICATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)885-9300
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS: XXXXXX US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.

Matches

ν, Gaps

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Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Seatent No. 5569830
GENERAL INFORMATION:
APPLICANT: BENNETT, Alan
APPLICANT: LABAVITCH, John M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLONE: pT2gpt-F1s
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1399 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYGTACCA 1440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-238-163-5 STANDARD; DNA; UNC; 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 CTTGAAAANTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 CTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 CTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 GTCCTCCTCTTGACCCTTCGTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAA 131
                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 19.7%;
Local Similarity 2.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: Sir
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
           SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                  REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 03-MAY-1994
                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                         94105-1493
                                                                                                                                              /AGENI III.
Bastian, Kevin L.
34,774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POWELL, Ann
STOTZ, Henrik
                                                                                         (415)
unknown
                                                                                                        (415) 543-9600
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                                                                                       543-5043
                                                                                                                                                                                                                                                            Release #1.0, Version #1.25
                                                                                                                                                                                                                                 US/08/238,163
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                                                                                                                                      2307E-540
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Best Local :
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OTHER INFORMATION: /standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP: 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/08388672A Sequence 22, Application US/08388672A Patent No. 5795961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-388-672A-22 STANDARD; DNA; UNC; 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 TGCAAAGTCATACCCGGCCCTGTTCCATGTGAGCTGCCAAGGAGGGTCAAGAGGAGGACA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 RYGTGTKSNV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 YGSSKTAMTSRNRTGKTANNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGSKNNGDRNN 179
                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YSSANYNYGGNNYGAAKTHYYTHTNYSGADSKTYTDSYNASGTSSSNGGTD-GNRSGADS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 cccGGTGGCC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MINVIMSSSSVVSRTASCNDKAKKDGNITSSWIIDCCNRTWGVCDIDIIYRVNNDSGHNK 60
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION UNMER: US/O8/388,672A
FILING DATE: 14-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: APPLICANT:
                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5795961man
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 212-688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Recombinant Human Anti-Lewis
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                             COUNTRY: UZIP: 10022
                                                              TELEFAX: 212-838-3884
                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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Similarity 14.7%;
28; Conservative
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Kitamura, Kunio
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Old, Lloyd J.
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5 Third Avenue
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Best Local Similarity 19.3%;
                                           SEQUENCE 215
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Sequence 5, Application US/08238163
Patent No. 5569830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
SEQUENCE 965 BP; 192 A; 170 C; 226 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-238-163-5 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XXXXXX
                                                                                                                                                           TELEFAX: (415) 543-50 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   905 THGNGNTYYWYKGKAKYRVSNRSGVSRSGSGSGTDYTTSSDATYYCGTHARTGGTKVKG 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        845 SVTAADTAVYYCVRGRSYDSDGGDYWGGTTVTVSSHUVKDMTSSSSASVGDRVTTCRSST 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 GACC-CTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                           MOLECULE TYPE: FEATURE:
                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: POWELL, Ann
APPLICANT: STOTZ, HENYIK
TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                  NAME/KEY: misc_feature
LOCATION: 1..215
OTHER INFORMATION: /standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
ENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                     APPLICATION NUMBER:
FILING DATE: 03-MAY
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTCCATCCCAGGAGCGCAGTGGCCACTAIGGGGTCTGGGCTGCCCCTTGTCCTCCTCTT 82
                                                                                                                                                                                                 NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 23
                                                                                                                                                                                                                                                                                                                                                  STREET: Steuart Stre
CITY: San Francisco
STATE: California
                                                                                                              TOPOLOGY:
                                                                                                                     STRANDEDNESS:
                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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     Similarity
22; Conser
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     Conservative
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                                                                                                                                                         (415) 543-5043
(415) 543-5043
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LABAVITCH, John M.
                                                                                                              unknown
                                                                                                  protein
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            11.3%;
                                                                                                                    single
                                                                                                                                                                                                                                                         US/08/238,163
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  Score 27; DB 1; L
Pred. No. 2.69e-04;
42; Mismatches 45
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Pred. No. 1.18e-06
53; Mismatches 4
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                                                                                                                                                                                                                                                                             Version #1.25
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   45; Indels
                    Length 215;
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 965 base pairs
TYPE: nucleic acid
STRANNEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic) SEQUENCE 965 BP; 192 A; 170 C; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22, Application US/08388672A
Sequence 22, Application US/08388672A
Patent No. 5795961
                                   841 NSRSSVTAADTAVYYCVRGRSYDSDGGDYW 870
                                                                      124 GTCATACCCGGCCCTGT-TCCATGTGAGCTGCCAAGGAGGGTCAAGAGGAGGACAAGGGG 66
                                                                                                781 GURHUVHVSGGVRSTSTCTASDYTTSYWGWVRGRGWGDYGGGYTNYNGKRGRYTMADTSS 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-388-672A-22 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 CTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAA 197
65 CAGCCCAGACCCCATAGTGGCCACTGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 THYYTHTNVSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSYGSSKTAM 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 CCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTG-AAGGAGT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 CNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSANYNYGGNNVGAAK 77
                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Recombinant Human Anti-Lewis
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Welt, Sydney APPLICANT: Kitamura, Ku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: LU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hanson, No. 57
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 14-FEB CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 805 Third Avenue CITY: New York STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
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                                                                                                                                                            Conservative
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Harris, William J
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Old, Lloyd J.
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                                                                                                                                                                               10.9%;
17.8%;
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14-FEB-1995
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Pred. No. 1.01e-03;
43; Mismatches 30
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                                                                                                                                                       Mismatches
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PCT-US95-11934-99 STANDARD; DNA; UNC; 75 BP.

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TELEFAX: (212) 869-9741/8864
TELEX: 6614 PENNIE
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 Dase pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIAN RE-BEASE #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934

FILING DATE: 20-SEP-1995

CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 99, Application PC/TUS9511934 Sequence 99, Application PC/TUS9511934 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 75 BP; 1 A; 1 C; 7 G; 5 T; 61 OTHER.
                                                                                                                 Sequence 98, Application PC/TUS9511934
Sequence 98, Application PC/TUS9511934
GENERAL INFORMATION:
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                                                                                                                                                                              PCT-US95-11934-98 STANDARD; DNA; UNC; 81
                                                                                                                                                                                                                             114 CCGGGTATG 122
                                                                                                                                                                                                                                                    65 NBGGTTGTG 73
                                                                                                                                                                                                                                                                       54 GGGTCTGGGCTGCCCCTTGTCCTCCTTGACCCTCCTTGGCAGCTCACATGGAACAGGG 113
                                                                                                                                                                                                                                                                                                                                   Local Similarity
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TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                 NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennle & Edmonds
STREET: 1155 Avenue of the Americas
                                                                               APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Bir
TITLE OF INVENTION: Peptide Lik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
 STATE: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                    CITY: New York
                                                                                                                                                                                                                                                                                                                         9
New York
Y: USA
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1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                     9.28;
                                                                   Antigen Binding Peptides (Abtides) From Peptide Libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18,872
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                                                                                                                                                                                                                                                                                                                                     Score 22; DB 4; Length 75; Pred. No. 1.67e-01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHANE: (212) 869-9741/8864
TELEY: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LEMOTH. 81 Nosconsites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic) SEQUENCE 81 BP; 6 A; 6 C; 4 G; 5 T; 60 OTHER.
                                                                                                                                                                                                                                                                                                                            Sequence 97, Application PC/TUS9511934 Sequence 97, Application PC/TUS9511934 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                              PCT-US95-11934-97 STANDARD; DNA; UNC; 82 BP
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TOPOLOGY: line
MOLECULE TYPE: I
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COMPUTER READABLE FORM:
MEDDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 NNVNNV 70
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATMAE: Misrock, S. Leslie
RESISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                        APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 20-SE CLASSIFICATION:
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 TELEPHONE:
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                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                       10036
                                                                                                                                                                                                                             New York
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ilarity 7.6%;
Conservative
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1155 Avenue of the Americas
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(212) 790-9090
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Pred. No. 1.67e-01;
20; Mismatches 41
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Sequence 1, Application US/0841844A
Sequence 1, Application US/0841844A
Patent No. 5773688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
SEQUENCE 82 BP; 1 A; 2 C; 10 G; 8 T; 61 OTHER.
                                                                                                                                         TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 97:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 GGGTCTGGGCTGCCCCTTGTCCTCCTTGACCCTCCTTGGCAGCTCACATGGAACAGGG 113
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP HEI 6-71048
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COLOR OF THE TOTAL OF T
                                                                                                                                                                                                       NAME: Oblon, NO. 5773688man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2589-024-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KURODA, HISAO
APPLICANT: HIROTA, NAOHIKO
APPLICANT: HIROTA, NAOHIKO
APPLICANT: ITO, KAZUTOSHI
TITLE OF INVENTION: GENE EXPRESSION VECTOR USING THE GENE
TITLE OF INVENTION: EXPRESSION REGULATING REGION OF THE ADD RIBOSYLATION
TITLE OF INVENTION: FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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                                       STRANDEDNESS: doub
                                                                              TYPE: nucl
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                                                                                           3088 base pairs
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                                                      double
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JEFFERSON DAVIS HIGHWAY, SUITE 400
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Pred. No. 1.67e-01
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Best Local S
Matches 3
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Best Local 9
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                      XXXXXX
                                    US-08-471-052A-144 STANDARD; DNA; UNC; 66
                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA
SEQUENCE 65 BP; 3 A; 3 C; 3 G; 2 T; 54 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 145, Application US/08471052A
Sequence 145, Application US/08471052A
Patent No. 5675033
GENERAL INFORMATION:
APPLICANT: Kay B K.
APPLICANT: Fowlkes, D. M.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,052A
FILING DATE: 06-JUNE-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                            61 CCTGG 65
                                                                                                                                                                                                                                                        Match 8.8%;
Local Similarity 13.8%;
es 9; Conservative
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Local Similarity 72.08;
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LENGTH: 65 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New Yor
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                                                                                                                                                                                                                                                                                                          Score 21; DB 1;
Pred. No. 5.69e-01
16; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 22; DB 3;
Pred. No. 1.67e-01
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 144:
                                                                                                                                                                                                                                                              Sequence 143, Application US/08471052A Sequence 143, Application US/08471052A Patent No. 5625033
                                                                                                                                                                                                                                                                                                                                              US-08-471-052A-143 STANDARD; DNA; UNC; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA
SEQUENCE 66 BP; 2 A; 3 C; 4 G; 2 T; 5S OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEGIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,052A
FILING DATE: 06-UNE-195
CLASSIFICATION: 530
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 5625033
GENERAL INFORMATION:
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Sequence 144, Application US/08471052A
                                                                                                                                                                                                                                                                                                                                  XXXXXX
                            CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Total
NUMBER OF SEQUENCES: 166
                                                                                                                                                                                                                                                                                                                                                                                                              41 AGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCCTTGACCCTCCTTGGCAGC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
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TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 166
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APPLICANT: Fowlk
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LENGTH: 66 bases
                                                                                                                                                                CORRESPONDENCE ADDRESS:
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TOPOLOGY: un
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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1155 Avenue of the Americas
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5.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                    XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-471-052A-142 STANDARD; DNA; UNC; 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 CTGGACTCATAGGAGGAATTTGTCAGAAAAGACTCCTTCAGCTTCAGTTGCAAAGTCATA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212 859-8864,
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 cccsc 114
TELEPHONE: 212 790-9090
TELEPAX: 212 865-8664/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 142
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Local Similarity 13.8%;
nes 9; Conservative
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APPLICANI: Kay, B. K.

APPLICANI: Fowlkes, D. M.

TITLE OF INVENTION: Totally Synthetic Affinity Reagents

TITLE OF INVENTION: 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9990
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,052A
FILING DATE: 06-JUNE-1995
                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 68 bases
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ATTORNEY/AGENT INFORMATION:
                                             REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
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MEDIUM TYPE: Floppy
                                                                                                      CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION:
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                                                                                REGISTRATION NUMBER:
                                                                                                                             APPLICATION NUMBER: US/08/471,052A FILING DATE: 06-JUNE-1995
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                                                                                             Misrock, S. Leslie
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Pred. No. 5.69e-01;
16; Mismatches 40
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Best Local :
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TELEX: 66141 PENNITE
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP; 3 A; 4 C; 3 G; 1 T; 63 OTHER.
                         XXXXXX
                                       PCT-US95-11934-100 STANDARD; DNA; UNC; 74 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOKET NUMBER: 1101-196-228
REFERENCE/DOKET NUMBER: 100-196-228
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Sequence 94, Application PC/TUS9511934
GENERAL INFORMATION:
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                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 8.8%;
Local Similarity 5.2%;
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TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: unknown
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STREET: 1155 Avenue of the Americas
CITY: New York
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Pred. No. 5.69e-01
20; Mismatches 3
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                                                                                                                                                                                                                                           39; Indels
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Best Local Similarity
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                     MOLECULE TYPE: DNA (genomic) SEQUENCE 74 BP; 6 A; 6 C; 1 G; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 100, Application PC/TUS9511934
Sequence 100, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding
TITLE OF INVENTION: Peptide Librari
                                         125 AGTCATACCCGGCCCTGTTCCATGTGAGCTGCCAAGGAGGGTCAAGAGGAGGACAAGGGG 66
65 CAGCCCA 59
                     65 NACCACA 71
                                                              REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ANDELOATION WINTER
                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: II.
STREET: New York
CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 20-SECLASSIFICATION:
                                                                                                                                                                                                                                                         TELEPHONE:
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                                                                                            Conservative
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                                                                                                                                                                                                                                                           790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigen Binding Peptides (Abtides) From
Peptide Libraries
103
                                                                                                                                                                                                                                                                                                                                                      PCT/US95/11934
                                                                                        Score 21; DB 4; Length 74; Pred. No. 5.69e-01; 19; Nismatches 43.
                                                                                                                                       1 T; 60 OTHER
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SUMMARIES SUMMARIES Description 252 17 AA754459 97SN1787 Rice Imm 252 17 AA754459 97SN1787 Rice Imm 252 17 AA754459 97SN1784 Rice Imm 247 17 AA754458 97SN1784 Rice Imm 247 17 AA754458 97SN1784 Rice Imm 247 17 AA754458 97SN1784 Human mf 2275 20 AF034173 AF034173 Human mf 2275 20 AF034173 Human mf	ariance 2.100; scal f results predicted al to the score of t s of the total score	Database: emb1-est58 1:em_est10 2:em_est11 3:em_est17 4:em_est18 5:em_est2 6:em_est9 7:em_gss1 Database: 8:gb_est9 10:gb_est1 11:gb_est12 12:gb_est 13:gb_est14 14:gb_est15 15:gb_est16 16:gb_est17 17:gb_est18 18:gb_est19 19:gb_est2 20:gb_est20 21:gb_est18 18:gb_est19 19:gb_est2 20:gb_est20 21:gb_est18 18:gb_est2 20:gb_est20 24:gb_est20 21:gb_est21 22:gb_est20 27:gb_est20 24:gb_est20 21:gb_est20 30:gb_est20 31:gb_est20 32:gb_est20 34:gb_est20 30:gb_est0 31:gb_est0 31:gb_est0 30:gb_est0 30:gb_est0 31:gb_est0 30:gb_est0 30:gb	<pre>Searched: 2883791 seqs, 1171580779 bases x 2 Post-processing: Minimum Match O% Listing first 45 summaries</pre>	STD : Dbase 0; Query 0	Title: >US-09-092-296-1 Description: (1-239) from US09092296.seq Perfect Score: 238 N.A. Sequence: 1 GGCCACCGGGACTTCAGTGTCCCTTCAGC Comp: CCGGTGGCCCTGAAGTCACAGGGAAGTCC Scoring table: TABLE default Gap 6	ase 3.1A John F. Collins, Biocomputing Research right (c) 1993-1998 University of Edinburgh, University of Edinburgh Acc	**************************************
Pred. No. nature 1.50e-56 no-UI. 1.52e-51 nature 2.04e-27 nature 1.76e-18 NA (T 1.49e-15 NA (T 3.49e-10 Zed i 2.31e-06 sells 3.76e-05 um II 3.76e-05	to have a being printed,	5:em_est2 2 12:gb_est13 st17 t20 t20 st24 st24 st24 5 33:gb_est6 38:gb_est6			.CCCTTCAGGGACCAGCGTCA 239 .GGGAAGTCCCTGGTCGCAGT	T.K. an algorithm Seconds cell updates/sec	(ML)

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AF035	B1934	B0154	AA14067	AG015	N3702	R61539	AA898	AA23996	H41	B45020	AI398	AA04699	AA82267	AI50953	W13114	AQ44421	AQ375	AI16031	T4741	F1005	M7952	AA335	B1258	AI 063	C2849	W79098	AA730	F08	D4 039	AF03	AA49848	T15255	AA76	W3387	
lmonella typhimuriu	2711-Sp6.1 TAMU	SRL-133c3-u	462.5prim	omo sapier	d03.s1 So	f01.sl Soares	M6Ğ7T7 Mycelial	w24g07.rl Soares n	1c01.s1 Soares	060-B1-B01-MF.abi	4B8T7 Subtracted	.rl Soares r	f01.rl Soares 2	h04.yl Soares	6e10.rl Soares	c0313 Trypand	11-161H11.TV RPCI	6d04.x1 Soares_fe	3f12.r1 Stratage	39H122 normalized	T00065 Mixed stage	9832 Epididymus H	Oll-Sp6.1 IGF Arab	2423.5prime GH Dro	493 Rice callus cD	5hl0.rl Soares fet	2c07.sl NCI CGAP	1DB011 normal	CS2342A Rice shoot	F038250 Human mRNA	h44b06.rl Barstead	rs855 lambdaZAPST F	1b05.s1 Soares_tes	03.rl	
7.76e-03	.76e-	.76e-	.76e-	.76e-	.76e-	.76e-	.76e	.76e-	.76e	766	766	. 76e	766	76e	7 6e	760	.76e	.76e	. 76e	76e	. 76e	.76e	65e	. 65e	. 65e -	656-	656-	. 65e-	656	.76e-	.76e-	.76e-	. 76e	.76e-	

ALIGNMENTS

FEATURES Source		COMMENT				REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	NID	ACCESSION	DEFINITION	Locus	RESULT 1
Fax: 82 331 290 0307 Email: myeun@sun20.asti.re.kr Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr Seq priner: M13 Reverse Primer. Seq priner: M13 Reverse Primer. 1252 /organism="Oryza sativa"	Contact: Eun M.Y. Department of Cytogenetics National Inst. of Agri. Sci. and Tech, RDA Suwon, Kyunggido, Korea Tel: 82 331 290 0301	On Jan 14, 1998 this sequence version replaced gi:1797457.	Large-scale Sequencing Analysis of ESTs from Rice Immature Seed	<pre>Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y., Lee,M.C. and Eun,M.Y.</pre>	Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,	Poaceae; Oryza.	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;	Oryza sativa	Oryza sativa.		AA754459.1 GI:2801165	92801165	CDNA Clone 97SN1787, mRNA sequence.	ZAPII CDNA Libr	AA754459 252 Dp mRNA EST 20-JAN-1998	

BASE COUNT ORIGIN

Ma tches

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Query Match
Best Local :
                                                                                  source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 TTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAANTCTGCCTC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 WBHYNTKCTASGWHTSTNYDVKS-STNTWGVTBSYDKSMHGYWCSBBVKYHTKV-STTRA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 CCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 BNTKVDVGNHTRCSRWRBVTRMAH-YHDYTNCBBYNNNDYHMWHBBMYBBTGCMTCTMWC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 TCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCCTCTTGACCCT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 YBCHGNBWWVCVASHGNYMSVHNCTBRGTHCDCKNVNWSTMTWGTVNWBNVSGDWHYWBV 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRSYTCVRKYCVMWMTKKVVKKYHVVBBGCH 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Letheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 328)
Bonaldo, M.F., Lennon, G. and G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AII36523 328 bp mRNA EST 11-FEB-1999 UI-R-C2p-ng-e-02-0-UI.S1 UI-R-C2p Rattus norvegicus cDNA clone UI-R-C2p-ng-e-02-0-UI 3', mRNA sequence.
                                                                                                                                                                                     The sequence tag present in the cDNA between the NotI site and the Oligo-dT track served to identify it as a clone from the normalized adult Lung library, cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res. 6 (9), 791-806 (1996)
97044477
                                                                                                                                                                                                                                                                                                                            Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Jan 14, 1998 this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two appr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Norway rat.
Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 23.9%;
Similarity 11.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Soares, MB
                                                                                                                                   Seq
                                                                                                                                                                                                                                                                                                  Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                   primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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/note="Yector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhOI; Directional CDNA library inserted into lambda ZAPII vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tlssue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
21 c 12 g 35 t 179 others
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                          /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:3637300
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Pred. No. 1.50e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               approaches
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Rattus.
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200

RESULT LOCUS

DEFINITION

KEYWORDS SOURCE

ORGANISM

VERSION ACCESSION

REFERENCE

JOURNAL MEDLINE AUTHORS TITLE

REFERENCE AUTHORS

COMMENT

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KEYWORDS VERSION RESULT LOCUS

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ACCESSION DEFINITION ę 밁 f ORIGIN BASE COUNT

Matches

FEATURES

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Query Match
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                                                                                         Contact: Eun M.Y.
Department of Cytogenetics
National Inst. of Agri. Sci.
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                           Poaceae; OTYZA.

1 (bases 1 to 252)

1 (bases 1 to 252)

Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P., Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y., Lee,M.C. and Eun,M.Y.

Lace,M.C. and Eun,M.Y.

Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)

On Jan 14, 1998 this sequence version replaced gi:1797457.
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Oryza sativa
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AA754459.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA clone
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
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/clone_lib="UI-R-C2p"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="PH10B (Life Technologies)"
/lab_host="98 g 91 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 791-806, 1996)"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 bp mRNA E ice Immature seed Lambda ZAPII 97SN1787, mRNA sequence.
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74.2%;
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Pred. No.
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1.62e-51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 WBHYNTKCIASGWHTSTNYDVKSSTNTWGVTBSYDKSMHGYW-C-SBBVKYHTKVSTTRA 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 TRSYTCVRKYCVMWMTKKVVKKYHVVBBGCHBTD 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 TTCCATGTGAGCTGCCAAGGAGGGTCAAGAGGAGGACAAGGGGCAGCCCAGACCCCCATAG 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 VBNTKVDVGNHTRCSRWRBVTRMAHYHDYTNCBBYNNNDYHMWHBBMYBBTGCMTCTMWC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 SYBCHGNBVWVCVASHGNYMSVHNCTBRGTHCDCKNVNWSTMTWGTVNWBNVSGDWHYWB 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92801164
AA754458.1
EST.
                                                                                                                           Department of Cytogenetics National Inst. of Agri. Sci. Suwon, Kyunggido, Korea Tel: 82 331 290 0307
                                                                                                                                                                                                                                                                                                     Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P., Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y., Lee,M.C. and Eun,M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA754458 247 bp mRNA EST 20-JAN-1998 97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa CDNA cione 97SN1784, mRNA sequence.
                                                     Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Koraa. 449-728 bhnahm@bioserver.myongji.ac.
Seq primer: M13 Reverse Primer.
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Similarity 9.8%;
21; Conservation
                                                                                                                                                                                                                                                                                                                                                                                       Poaceae; Oryza.
                                                                                                                                                                                                                                                     Jan 14, 1998 this sequence version replaced gi:1797455.
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/organism="Oryza sativa"
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/tissue_type="Immature Seed"
/dev_Stage="5 days after pollination"
/lab_host="E. coli SOLR"
21 c 12 g 35 t 179 others
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XhOI: Directional CNNA library inserted into lambda %APII
Vector at $\frac{\text{s}'}{\text{end}}$ with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
                                   Location/Qualifiers
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/clone="97SN1787"
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/cultivar="Milyang23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 51; DB 17;
Pred No. 1.52e-46;
                                                                                                                                                                                   and Tech,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 252;
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Best Local
                                                                                        Source
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154 NGTSAT-KRVTGYDKTDSDCGGGCWRKVTYGSS-BYBRCGVNVMVRTTSMWTDKSTKMBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 TGTGAGCTGCCAAGGAGGGTCAAGAGGAGGACAAGGGGGCAGCCCCAGACCCCATAGTGGCC 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 GYGKTTYNYHSGWNNRCSNSYYYWBTAYCDYBHYBDRANHYDDTRCTNDRGYCNYTASD 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 VRRYGTTINNGKHNGRTTIWNDCSDNAHCRYTYBWYYARSKYGYGTBYYSWNVDTNTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAATTTGTCAGAAAAGACTCCTTCAGCTTCAGTTGCAAAGTCATACCCGGCCCTGTTCCA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGAGATGGAGGAGGCAGANTTTTCAAGCAATTCCAGGAAGCTGGACT-CATAGGAG 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa

Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta; euphyllophytas: Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
On Jan 14, 1998 this sequence version replaced gi:1797455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 247)
1 (bases 1 to 247)
Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P., Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y., Lee, M.C. and Eun, M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA754458 247 bp mRNA
97SN1784 Rice Immature Seed Lambda
cDNA clone 97SN1784, mRNA sequence,
AA754458
                                                                                                                                                                                               Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac..
Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                   Suwon, Kyunggido, Ko
Tel: 82 331 290 0301
Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                  Department of Cytogenetics
National Inst. of Agri. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Eun M.Y.
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/organism="Oryza sativa"
/cultivar="Milyang23"
/cultivar="Milyang23"
/note="Yector: pBlueScript SK(+); Site_1: EcoRI; Site_2:
XhOI; Directional CDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with XhO I site."
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/note="Yector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda 2AFI
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
                                                                                                                                                                             ocation/Qualifiers
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Pred. No. 2.04e-27;
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Best Local Similarity 13.3%;
Matches 26; Conservative
                                                                        Matches
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                                   1480 RYKRWKRRKGRRKRMTGMYKRMYRAMMAMCAMMACWWYYWKMRGMKKCWKYRKYKKYTS 1539
                                                                                                                                                                                                                                                                                        source
217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 MBNKKRGMSRNWTDTK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 KTDSDCGGGCWRKVTYGS-SBYBRCGVNVMVRTTSMWTDKSTKMBSMDMSRRSRVHYGRW 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 GACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 GRTTTWNDCSDNAHCRYTVBWYYARS-KYGYGTBYYSWNVDTNTGGTGVGKTTVNVHSGW 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 TIGTCCTCCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGT-ATGACTTTG 128
                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGCTTGAAAANTCTG 204
ATGGAGGAGGAGGCAGANTTTTCAAGCAATTCCAGGAAGCTGGACTCATAGGAGGAATTT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2275)

Tripodis, N. and Ragoussis, J.

Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                          Guys Hospital
7th floor, Guy's Tower, London SE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF034173 2275 bp mRNA EST AF034173 Human mRNA (Tripodis and Ragoussis) Clone ntcon2 contig, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                   Division of Medical and Molecular Genetics
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                                                                                                                                                                                                                                                                                                                               Email: nikos@nki
                                                                        Similarity 9.6% 11; Conservative
                                                                                                                                                                         438
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                           19, 1998 this sequence version replaced g1:2045115
                                                                                                                                                                                                                                                                                                                                                                                                        Tripodis, Nikos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:4530"
/map="6"
/clone="97SN1784"
/clone_1b="Rice Immature Seed Lambda ZAPII cDNA Library"
/tlssue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coll SOLR"
/lab_host="E. coll 30LR"
                                                                                                                                                            /clone="ntcon2 contig"
/clone_lib="Human mRNA (Tripodis and Ragoussis)"
/clone_lib="Human mRNA (Tripodis and Ragoussis)"
                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="6p21.3"
                                                                                                                                                                                                                                                                                      Cocation/Qualifiers
                                                                                          13.0%;
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Pred. No. 1.76e-18;
88; Mismatches 79
                                                                      Score 31; DB 20;
Pred. No. 1.24e-15;
64; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                9RT, UK
                                                                          39;
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                                                                                                             Length 2275;
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Best Local
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                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1615 WITWWYMW 1622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1556 YWYCWCCTSMKSASCAMMRWMGYMGS-RSSRSYWGYWGSMSGCYGMTKRYYRYSWTGWTK 1614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 GTCAGAAAAGCTCCTT-CAGCTTCAGTTGCAAAGTCATACCCGGCCCTGTTCCA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 CTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                84 ACCCTCCT
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1 (bases 1 to 2275)

Tripodis, N. and Ragoussis, J.

Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF034173 2275 bp mRNA EST 30-MAR-1998 AF034173 Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 348)

Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Kabaktchis,C. and Tessler,A.

IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                  F06958.1
EST.
                                                                                                                                                                                                                                                                                                              F06958 348 bp mRNA EST 20-FEB-1995 HSC10C101 normalized infant brain cDNA Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guys Hospital
7th floor, Guy's Tower, London
Email: nikos@nki.nl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Tripodis, Nikos
Division of Medical and Molecular Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
Qn Jan 19, 1998 th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 11.3%;
Similarity 16.2%;
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its expression
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                                                                                                                                                                                                                                                                                           mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="ntcon2 contig"
/clone_lib="Human mRNA (Tripodis and Ragoussis)"
619 c 470 g 599 t 149 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="6p21.3"
                                                                                                                                                                                                                                       GI:672595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    this sequence version replaced
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Pred. No. 3.49e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
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VERSION
KEYWORDS
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ACCESSION
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AUTHORS
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Best Local
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MEDLINE
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

ACE 1 (bases 1 to 238)

RS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Wan-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.B.Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palanques,R.F., McDonald,L.A., Nugven,D.T., Pelligrino,S.M.,
Phillips,C.A., Kyder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Collenan,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78
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nes 45; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
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EST88915
AA376266
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95277534
On Sep 2
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High quality sequence stop: 150.
Location/Oualifiers
                                                                                                                                                                                                                                                                                                                                                              human.
                                                                                                                                                                                                                                                                                                                                                                                                    AA376266.1
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1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21, 1992 this sequence version replaced gi:279286
                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 bp mRNA EST 21-APR-1997
HSC172 cells II Homo sapiens cDNA 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism-"Homo sapiens"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="total brain"
/dev_stage="3 months old"
91 c 90 g 81 t
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/db_xref="taxon:9606"
/clone="c-1qc10"
/clone=lib="normalized infant brain cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                    GI:2028809
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Pred. No. 2.31e-06;
0; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           it: C; Genexpress_sequence_idt: ylc-lqc10
std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 CTCTTGA 84
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, M.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehn, C.L., Hanna, M.C., Hedblom, E., Hinkle, P. S.Jr.,
Glodek, A., Gnehn, C.L., Hanna, M.C., Hedblom, E., Hinkle, P. S.Jr.,
Kelley, J.M., Kelley, J.C., Liu, L. I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Beddarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
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EST26816
                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa,
Eutheria; Primates,
l (bases l to 311)
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA323964.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: M13 Reverse
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similarity 67.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 3018699056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: lung; Vector: pBlue
ECORI; Site_2: XhOI"
/db_xref="AGCC (inhost):180944"
/db_xref="taxon:9606"
/clone_lib="HSC172 cells II"
/cell_type="fibroblast"
/cell_tine="HSC172 (60PDL)"
/dev_stage="fetal"
8 a 70 c 50 g 66 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 bp mRNi
Cerebellum II Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Oualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:1976290
                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 23; DB 12; L, Pred. No. 3.76e-05; 0; Mismatches 22;
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sapiens cDNA 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vector: pBluescript SK-; Site_1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
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COMMENT

JOURNAL MEDLINE

TITLE

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Query Match
Best Local S
Matches 2
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96026280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dilllon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                         Mus musculus

EukaryOta; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Euthoria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 364)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Moore,B.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g1315794
w33870.1
                                     Contact: Marra M/Mouse EST Project Washin-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Lc Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mc56b03.rl Soares |
clone IMAGE:352493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9712 Medical Center Drive, Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research 9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Apr 14, 1993 this sequence version replaced gi:693635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Kerlavage, AR
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                               Unpublished (1996)
On May 18, 1995 th
                                                                                                                                                                                                                                    Waterston, R.
The WashU-HHMI Mouse EST Project
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Similarity 89.7%;
26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="organ: brain; Vector: pBlueScript SK-; Site_1:
ECORI; Site_2: XhoI"
/db_xref="ATCC (inhost):124516"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Clone_lib="Cerebellum II"
/tissue_type="cerebellum"
/dev_stage="adult"
110 c 74 g 64 1
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                                                                                                                                                                                          this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mouse embryo NbME13.5 14.5 Mus musculus cDNA 35', mKNA sequence.
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Pred. No. 3.76e-05;
0; Mismatches 3
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                                                                                      Louis,
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST
  Insert Length: 691 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quallty sequence stop: 402.
Location/Qualifiers
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SOURCE ORGANISM

KEYWORDS ACCESSION ERSION

REFERENCE

AUTHORS

COMMENT

TITLE JOURNAL

RESULT LOCUS

DEFINITION

Ş 뭥 BASE COUNT ORIGIN

FEATURES

source

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282 AACTGAAAGGGAAGGAGGCTTTTTCCCACATATTTCTCCCT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 AACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:224293
Seq primer: ETPrimer
High quality sequence stop: 360.
                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 412)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
AA769782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA769782 412 bp mRNA
ah71b05.sl Soares_testis_NHT
                 CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                      Email: Robert_Strausberg@nih.gov cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                           On Jan 9, 1998 this sequence version replaced g1:936203
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA769782.1 GI:2821020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 9.7%;
Similarity 79.5%;
31; Conservative
www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M.Fatima Bonaldo. "
/db_xref_Mtaxon:10090"
/clone="Inface:352493"
/clone_lib="Soares mouse embryo NbME13.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tlssue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/dev_stage="19.10B"
/lab_host="pH10B"
73 c 87 g 104 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 23; DB 34;
Pred. No. 3.76e-05;
0; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens cDNA clone 1321041 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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                                                                                                                                                                                                                                                                                            Project (CGAP),
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                                                                                                                               Fatima
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ORIGIN

Query match Best Local S Matches 4

BASE COUNT

111

Дb ç DЬ

322 GGCAACA 328

24 GGAGACA 18

DEFINITION

RESULT

13

T15255

ACCESSION

sequence. T15255

ERSION

Gaps

0;

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y Match 9.7%;
Local Similarity 67.2%;
hes 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Carnegie Institution
Carnegie Institution, 290 Panama
Tel: 4153251521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l (bases 1 to 426) vandeLoo.F.J.. Turner.S. and Somerville,C. Expressed sequence tags from developing castor seeds Plant Physiol. 108, 1141-1150 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              crs855 lambdaZAPST Ricinus communis cDNA clone pcrs855, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; Euphorbiales; Euphorbiaceae; Ricinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g688907
T15255.1 GI:688907
                                                                                                                                                                                                                                                                                                                                                                       Email: crs@andrew.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Somerville CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ricinus communis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                castor bean
                                                                                                                                                                                                                                                                                                                                                        primer: T3
            to the instructions of the manufacturer (Stratagene):
synthesis was primed from the poly(A) tail, and cloned
directionally into XhoI (3') and EcoRI (5') Sites. In few
cases, sequence data indicated that this directionality
was reversed. Partial cDNA clones predominate. "
                                                                                                                                 /organism="Ricinus communis"
/strain="Baker 296"
/strain="Paker 296"
/note="Vector: lambdaZAPII; Site_1: EcoRI; Site_2: XhoI;
Poly(A)+ RNA was purified from developing stage III to
stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760,
1982) endosperm plus embryo of immature castor fruits.
cDNA was synthesized and cloned into lambdaZAPII according
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Double-Stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7/73 vector. Library went through one round of normalization to Cot5, and was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/note="Vector: pf773D-rea (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; lst strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              constructed by Bento Soares and M. Fatima Bonaldo.
/db_xref="taxon:9606"
/clone="1321041"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="1321041"
/clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host-"DH10B"
78 c 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426 bp
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Pred. No. 3.76e-05;
0; Mismatches 22; Indels
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ORIGIN
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ORGANISM
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Best Local Similarity 71.4%;
Matches 35; Conservative
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1 (Dases 1 to 481)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Materston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA498488 481 bp mRNA EST 01-JUL-1997 vh44b06.rl Barstead mouse pooled organs MPLRB4 Mus musculus cDNA clone IMAGE:889811 5' similar to gb:M30514 Mouse muscle nicotinic acetylcholine receptor gamma-subunit (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicinep
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 53108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -28ml3 rev2 ET from Amersham H1gh quality sequence stop: 461. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dmail: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:517771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1996)
On Sep 12, 1996 this sequence version replaced g1:1405167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
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/clone_lib="lambdazAPST"
126 a 61 c 99 g 129 t
                                                                                                                                                                                                                       /clone_lib="Barstead mouse pooled
/sex-"mixed"
                                                                                                                                 /tissue_type="pooled organs"
/dev_stage="7 day"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="FVB/N"
9.7%;
76.7%;
                                                                                          _host-"DH10B"
  Score 23;
Pred. No.
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Pred. No. 3.76e-05;
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                                                                                          106
                 DB 14; Length 481;
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REFERENCE AUTHORS TITLE

JOURNAL

SOURCE KEYWORDS

EST

ORGANISM

FEATURES

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Search completed: Sun Oct 24 16:38:34 1999 Job time: 471 secs.
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                                                                                                                                                                                                                  Query Match 9.7%; Score 23; DB 20; Length 1287; Best Local Similarity 25.8%; Pred. No. 3.76e-05; Matches 24; Conservative 32; Mismatches 37; Indels
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                                                                  : | : :::||| :| :: :::||| 113 GCCGGGTATGACTTTGCAACTGAAGCTGAAGCA 145
                                                                                      441 STCMTHYNCCDCKTCGSAGVTVNHHDWSMAGGA 473
                                                                                                                                                                   381 VYVATCHAGSCCYACYTCBCDCBTGGGDTBSHBYCMCBCBANADGATBATCGKYGGYBGA 440 ::: || |:| :: :| |::::| |:: :| |:| :: :|
                                                                                                                                             53 GGGGTCTGGCCCTTGTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGG 112
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1287)
Tripodis,N. and Ragoussis,J.
Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 Chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     boundary
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2045085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF038250 1287 bp mRNA EST 30-MAR-1998 AF038250 Human mRNA (Tripodis and Ragoussis) Homo Sapiens cDNA clone ntcon9, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Tripodis, Nikos
Division of Medical and Molecular Genetics
Guys Hospital
7th floor, Guy's Tower, London SE1 9RT, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g2815880
AF038250.1 GI:2815880
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: nikos@nki.nl.
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                                                                                                                                                                                                                                                                                                                   349 a
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. 1287
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="5p21.3"
/clone="ntcon9"
                                                                                                                                                                                                                                                                                                             /Clone_lib-"Human mRNA (Tripodis and Ragoussis)"
219 c 293 g 361 t 65 others
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L27 ANSWER 1 OF 4 CAPLUS COPYRIGHT 1999 ACS

DUPLICATE 1

ACCESSION NUMBER:

1999:518247 CAPLUS

DOCUMENT NUMBER:

131:166197

TITLE:

Methods for detecting lung

diseases

INVENTOR (S):

Cohen, Maurice; Friedman, Paula

N.; Gordon, Julian; Hodges, Steven C.; Klass, Michael R.; Kratochvil, Jon D.; Roberts-Rapp, Lisa; Russell, John C.;

Stroupe, Steven D.

PATENT ASSIGNEE(S):

Abbott Laboratories, USA

SOURCE:

U.S., 36 pp., Cont.-in-part of U.S. Ser. No.

744,211, abandoned.

CODEN: USXXAM

DOCUMENT TYPE:

Patent

LANGUAGE:

English

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE ----

-----US 5939265 Α 19990817 US 1997-964725 19971105

PRIORITY APPLN. INFO.:

US 1996-744211 19961105 A set of contiguous and partially overlapping RNA sequences and polypeptides encoded thereby, designated as LU103 and transcribed from lung tissue are described. A fully sequenced clone representing the longest continuous sequence of LU103 is also disclosed. These sequences are useful in detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or detg. the predisposition of an individual to diseases and conditions of the lung such as lung cancer.

L27 ANSWER 2 OF 4 CAPLUS COPYRIGHT 1999 ACS

DUPLICATE 2

ACCESSION NUMBER:

1999:8152 CAPLUS

DOCUMENT NUMBER:

130:77055

TITLE:

Protein LS170 and cDNA sequences useful for

detecting diseases of the human

INVENTOR (S):

Billing-Medel, Patricia A.; Cohen, Maurice; Colpitts, Tracey

L.; Friedman, Paula N.; Gordon,

Julian; Granados, Edward N.; Hodges, Steven C.;

Searcher : Shears 308-4994

Klass, Michael R.; Kratochvil, Jon D.; Roberts-Rapp, Lisa; Russell, John C.;

Stroupe, Stephen D.

PATENT ASSIGNEE(S):

SOURCE:

Abbott Laboratories, USA PCT Int. Appl., 120 pp.

CODEN: PIXXD2

DOCUMENT TYPE:

Patent English

LANGUAGE: FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE -----______ WO 9856951 A1 19981217 WO 1998-US11601 19980611

W: CA, JP

RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

PRIORITY APPLN. INFO.:

US 1997-49183 19970611

A set of contiguous and partially overlapping cDNA sequences and polypeptides encoded thereby, designated as LS170 and transcribed from human lung tissue, is described. These sequences are useful for the detecting, diagnosing, staging, monitoring, prognosticating, in vivo imaging, preventing or treating, or detg. the predisposition of an individual to diseases and conditions of the lung, such as lung cancer. Also provided are antibodies which specifically bind to a LS170-encoded polypeptide or protein, and agonists or inhibitors which prevent action of tissue-specific LS170 polypeptides, which mols. are useful for the therapeutic treatment of lung diseases, tumors, or metastases.

L27 ANSWER 3 OF 4 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD

ACCESSION NUMBER: 1998-437479 [37] WPIDS

DOC. NO. NON-CPI: DOC. NO. CPI:

N1998-340776 C1998-133112

TITLE:

New nucleic acid for the lung

disease marker LU105 - polypeptides,

antibodies and genes, used for diagnosis,

prevention, treatment of lung disease, specifically cancer.

DERWENT CLASS:

B04 D16 S03

INVENTOR(S):

BILLING-MEDEL, P A; COHEN, M;

COLPITTS, T L; FRIEDMAN, P N;

GORDON, J; GRANADOS, E N; HODGES, S C; KLASS,

M R; KRATOCHVIL, J D; ROBERTSRAPP, L;

RUSSELL, J C; STROUPE, S D

PATENT ASSIGNEE(S):

(ABBO) ABBOTT LAB

COUNTRY COUNT:

19

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG _____

WO 9833926 Al 19980806 (199837) * EN 117

RW: AT BE CH DE DK ES FI FR GB GR IE IT LU MC NL PT SE

W: CA JP

APPLICATION DETAILS:

Searcher: Shears 308-4994

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	6			

PRIORITY APPLN. INFO: US 1997-791710 19970131

AN 1998-437479 [37] WPIDS

AB WO 9833926 A UPAB: 19980916

A method for detecting target LU105 nucleic acid (I) comprises treating a sample with at least one LU105-specific nucleic acid (II), or its complement. (II) is at least 50% identical with 190, 244, 225, 114, 562 or 519 bp sequences given in the specification, or their fragments and complements.

Also claimed are:

- (1) (I) or its fragments able to hybridise selectively to the LU105 gene and having at least 50% identity with the 190, 244, 225, 114, 562 or 519 bp sequences given above;
- (2) recombinant expression systems including (I) and control sequence;
 - (3) cells transformed with this expression system;
- (4) LU105 polypeptides (III) at least 50% identical with the 104, 26, 19, 21, 18 or 19 amino acid (aa) sequences given in the specification or their fragments;
- (5) antibodies (Ab) that bind to at least one LU105 epitope present in (III);
- (6) cells transformed with the 190, 244, 225, 114, 562 or 519 bp sequences described above;
 - (7) LU105 specific nucleic acid (II); and
- (8) genes, or their fragments, that encode a protein at least 50% identical with the 104 aa sequences as in (4).

USE - LU105 is a lung disease marker. Cells as in (3) are used to express recombinant (III) which are used to raise Ab. Ab are used to detect the LU105 antigen, and correspondingly this antigen is used to detect specific antibodies, in usual immunoassays. (I) and (III) are used for diagnosis, staging, monitoring, prognosis, prevention, treatment (e.g. using antisense molecules, ribozymes, Ab or other antagonists) and determination of susceptibility to, lung disease

, specifically cancer. (III) are also used to screen for specific binding agents, potentially useful therapeutically. LU105 is a marker for lung disease (present at high

concentration, in altered form or in an unusual body compartment).

ADVANTAGE - LU105 can be detected in blood, plasma or serum in an inexpensive, non-invasive test.

Dwg.0/6

L27 ANSWER 4 OF 4 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD

ACCESSION NUMBER: DOC. NO. NON-CPI: 1998-286957 [25] WPIDS

DOC. NO. CPI:

N1998-225472 C1998-088988

TITLE:

Lung tissue derived polynucleotide LU103 - useful to detect, diagnose, stage, monitor, prognose, prevent, treat or determine pre-disposition to lung disease, e.g. lung

cancer.

Searcher: Shears 308-4994

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DERWENT CLASS:

B04 D16 S03

INVENTOR(S):

COHEN, M; FRIEDMAN, P N;

GORDON, J; HODGES, S C; KLASS, M R;

KRATOCHVILL, J D; ROBERTS-RAPP, L; RUSSELL, J

C; STROUPE, S D

PATENT ASSIGNEE(S):

(ABBO) ABBOTT LAB

COUNTRY COUNT:

19

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG

WO 9820143 A1 19980514 (199825)* EN 86

RW: AT BE CH DE DK ES FI FR GB GR IE IT LU MC NL PT SE

W: CA JP

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9820143	A1	WO 1997-US20680	19971105

PRIORITY APPLN. INFO: US 1996-744211 19961105

AN 1998-286957 [25] WPIDS

AB WO 9820143 A UPAB: 19980715

The following are claimed: (1) a method for detecting the presence of a target LU103 polynucleotide in a test sample, comprising: (a) contacting the sample with at least 1 LU103-specific polynucleotide, and (b) detecting the target LU103 polynucleotide in the test sample, where the LU103 polynucleotide has at least 50% identity to the 269, 263, 225, 507 or 519 bp nucleic acid sequence given in the specification; (2) a method for detecting LU103 mRNA in a test sample, comprising: (a) performing reverse transcription with at least 1 primer in order to produce cDNA; (b) amplifying the cDNA using LU103 oligonucleotides as sense and antisense primers to obtain LU103 amplicon, and (c) detecting LU103 amplicon in the test sample, where the LU103 oligonucleotides utilised in steps (a) and (b) have at least 50% sequence identity to the 269, 263, 225, 507 or 519 bp sequence and (3) a method detecting a target LU103 polynucleotide in a test sample suspended of containing the target, comprising: (a) contacting the test sample with at least 1 LU103 oligonucleotide as a sense primer and at least 1 LU103 oligonucleotide as an anti-sense primer and amplifying to obtain a first stage reaction product; (b) contacting the first stage reaction product with at least 1 other LU103 oligonucleotide to obtain a second stage reaction product, provided that the other LU103 oligonucleotide is located 3' to the LU103 oligonucleotides utilised in step (a) and is complementary to the first stage reaction product, and (c) detecting the second stage reaction product as an indication of the presence of the target LU103 polynucleotide, where the LU103 oligonucleotides utilised in steps (a) and (b) have at least 50% sequence identity to the 269, 263, 225, 507 or 519 bp sequence; (4) a purified polynucleotide derived from an LU103 gene, where the polynucleotide is capable of selectively hybridising to the nucleic acid of the LU103 gene and has at least 50% identity to the 269, 263, 225, 507 or 519 bp

Searcher : Shears 308-4994

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sequence; (5) a recombinant expression system comprising a nucleic acid sequence that includes an ORF derived from LU103 operably linked to a control sequence compatible with a desired host, where the nucleic acid sequence has at least 50% identity to the 269, 263, 225, 507 or 519 bp sequence; (6) cell transfected with the recombinant expression system; (7) cell transfected with a nucleic acid sequence encoding at least 1 LU103 epitope, where the nucleic acid sequence has the 269, 263, 225, 507 or 519 bp sequence; (8) composition comprising a LU103 polynucleotide, where the polynucleotide has at least 50% identity to the 269, 263, 225, 507 or 519 bp sequence; (9) gene which encodes a LU103 protein which comprises an amino acid sequence with at least 50% identity with the 93 residue amino acid sequence given in the specification, and (10) gene comprising DNA having at least 50% identity with the 507 or 519 bp sequence.

USE - The methods and products of the invention may be used to detect, diagnose, stage, monitor, prognose, prevent, treat or determine the predisposition diseases and conditions of the lung, e.g. lung cancer.

Dwg.0/4

Searcher: Shears 308-4994

(FILE 'CAPLUS' ENTERED AT 12:09:17 ON 25 OCT 1999)

L1 10217 SEA ABB=ON PLU=ON LUNG(3A) (DISEAS? OR DISORDER)

L2 583 SEA ABB=ON PLU=ON L1(S)(IDENTIF? OR DETECT? OR DET##

OR DETERM? OR DIAGNOS?)

L3 14 SEA ABB=ON PLU=ON L2 AND (REAGENT OR EPITOPE OR LS147

OR LS 147)

L3 ANSWER 1 OF 14 CAPLUS COPYRIGHT 1999 ACS

ACCESSION NUMBER:

1999:556186 CAPLUS

TITLE:

Pigeon fanciers' lung: identification of disease

-associated carbohydrate epitopes on

pigeon intestinal mucin

AUTHOR (S):

Baldwin, C. I.; Todd, A.; Bourke, S. J.; Allen,

A.; Calvert, J. E.

CORPORATE SOURCE:

Department of Immunology, The Medical School,

University of Newcastle upon Tyne, Newcastle

upon Tyne, NE2 4HH, UK

SOURCE:

Clin. Exp. Immunol. (1999), 117(2), 230-236

CODEN: CEXIAL; ISSN: 0009-9104

PUBLISHER:

Blackwell Science Ltd.

DOCUMENT TYPE:

Journal

LANGUAGE:

English

Pigeon intestinal mucin, a complex high mol. wt. glycoprotein, is a key antigen in the development of pigeon fanciers' lung (PFL). We have studied the specificity of antibodies to mucin in patients with PFL and asymptomatic antibody-pos. individuals. Extensive papain digestion, which removes the non-glycosylated regions of the mucin leaving the heavily glycosylated "bottle brush" regions, resulted in a 600-fold decrease in IgG3 antibody titers with little effect on IgG1 and IgG2 titers. This suggests that IgG1 and IgG2 are directed against the region rich in O-linked sugar chains while the majority of the IgG3 is directed against epitopes which are proteinase-sensitive. Lectin mapping of the carbohydrates present on pigeon intestinal mucin demonstrated high levels of exposed N-acetyl neuraminic acid, N-acetyl galactosamine and N-acetyl glucosamine, with lower levels of fucose and some galactose. from pigeon fanciers inhibited binding of lectins specific for N-acetyl neuraminic acid, N-acetyl galactosamine, internal N-acetyl glucosamine and fucose. Sera from people with PFL, compared with sera from asymptomatic antibody-pos. fanciers, had significantly higher titers of antibody that inhibited binding of four lectins specific for N-acetyl galactosamine and one fucose-specific lectin, suggesting that these sugars may play a dominant role in disease-assocd. epitopes. The results suggest that different IgG subclasses recognize different epitopes on mucin and that the epitopes recognized by the major subclasses are present on the O-linked oligosaccharides. Further, the carbohydrate-specific anti-mucin antibodies produced by PFL Shears 308-4994 Searcher :

6.22

patients may differ in their specificity from those found in asymptomatic individuals.

L3 ANSWER 2 OF 14 CAPLUS COPYRIGHT 1999 ACS

ACCESSION NUMBER: 1

1999:8152 CAPLUS

DOCUMENT NUMBER:

130:77055

TITLE:

Protein LS170 and cDNA sequences useful for

detecting diseases of the

human lung

INVENTOR(S):

Billing-Medel, Patricia A.; Cohen, Maurice; Colpitts, Tracey L.; Friedman, Paula N.; Gordon, Julian; Granados, Edward N.; Hodges, Steven C.;

Klass, Michael R.; Kratochvil, Jon D.;

Roberts-Rapp, Lisa; Russell, John C.; Stroupe,

Stephen D.

PATENT ASSIGNEE(S):

Abbott Laboratories, USA PCT Int. Appl., 120 pp.

CODEN: PIXXD2

SOURCE:

Patent

DOCUMENT TYPE: LANGUAGE:

English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

W: CA, JP

RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

PRIORITY APPLN. INFO.:

US 1997-49183 19970611

As set of contiguous and partially overlapping cDNA sequences and polypeptides encoded thereby, designated as LS170 and transcribed from human lung tissue, is described. These sequences are useful for the detecting, diagnosing, staging, monitoring, prognosticating, in vivo imaging, preventing or treating, or detg. the predisposition of an individual to diseases and conditions of the lung, such as lung cancer. Also provided are antibodies which specifically bind to a LS170-encoded polypeptide or protein, and agonists or inhibitors which prevent action of tissue-specific LS170 polypeptides, which mols. are useful for the therapeutic treatment of lung diseases, tumors, or metastases.

L3 ANSWER 3 OF 14 CAPLUS COPYRIGHT 1999 ACS

ACCESSION NUMBER:

1998:674032 CAPLUS

DOCUMENT NUMBER:

130:64487

TITLE:

Immunohistochemical detection of multidrug resistance protein in human lung cancer and

normal lung

AUTHOR (S):

Wright, Scott R.; Boag, Alexander H.; Searcher : Shears 308-4994

Valdimarsson, Gunnar; Hipfner, David R.;

Campling, Barbara G.; Cole, Susan P. C.; Deeley,

Roger G.

CORPORATE SOURCE: Departments of Pathology and Cancer Research

Laboratories, Queen's University, Kingston, ON,

K7L 3N6, Can.

SOURCE: Clin. Cancer Res. (1998), 4(9), 2279-2289

CODEN: CCREF4; ISSN: 1078-0432

PUBLISHER: American Association for Cancer Research

DOCUMENT TYPE: Journal LANGUAGE: English

Monoclonal antibody QCRL-1 is highly specific for a defined linear epitope in a relatively poorly conserved region of the human multidrug resistance protein (MRP). The authors have used QCRL-1 to examine MRP expression in archival and fresh snap-frozen samples of untreated small cell (SC) and non-small cell (NSC) lung cancers (LCs), as well as normal lung. The authors found that the majority (87%) of all histol. subtypes of NSCLC had detectable levels of MRP in most of the tumor mass. In a substantial proportion of adenocarcinomas (55%) and squamous cell carcinomas (28%), immunoreactivity approached that obtained with the highly multidrug resistant cell line H69AR from which the MRP was originally cloned. Both the level and frequency of MRP expression in untreated SCLC was significantly lower than in NSCLC. The MRP was detectable in only 56% of SCLC tumors and, in most cases, was expressed in small focal clusters of cells. Immunofluorescence studies of tumor tissue and normal lung confirmed the plasma membrane location of the MRP. However, in normal bronchial epithelium and seromucous glands, unlike in tumor cells, the MRP was detected only on basolateral membranes. In addn., strong MRP immunoreactivity was detected in reactive type II pneumocytes present in hyperplastic alveoli, but not in normal type I and type II pneumocytes. No potentially confounding correlation independent of its possible role in drug resistance was obsd. between MRP expression in untreated NSCLC and any clinicopathol. parameter examd., including overall survival.

L3 ANSWER 4 OF 14 CAPLUS COPYRIGHT 1999 ACS

ACCESSION NUMBER: 1997:692333 CAPLUS

DOCUMENT NUMBER: 127:316564

TITLE: Diagnosis of chronic respiratory failure and

pulmonary emphysema, and diagnostic

reagents

INVENTOR(S): Okuda, Yukichi; Morita, Riichiro; Hanatani,

Mitsuya; Matsuo, Katsuhiko

PATENT ASSIGNEE(S): Toa Gosei Chemical Industry Co., Ltd., Japan

SOURCE: Jpn. Kokai Tokkyo Koho, 4 pp.

CODEN: JKXXAF

DOCUMENT TYPE: Patent LANGUAGE: Japanese

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FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE

JP 09274037 A2 19971021 JP 1996-104629 19960402

AB Detn. of human serum vascular endothelial growth factor/vascular permeability factor (VPF) is useful for accurate diagnosis of the title diseases. The detn. is carried out by using anti-VPF antibodies or VPF receptors. The serum level of VPF in patients with the diseases is much higher than healthy humans.

L3 ANSWER 5 OF 14 CAPLUS COPYRIGHT 1999 ACS

ACCESSION NUMBER: 1997:44677 CAPLUS

DOCUMENT NUMBER: 126:55930

TITLE: Detection of neoplastic cells based on

alternatively spliced transcripts of the p15INK4B and p16INK4A cyclin/CDK inhibitors

INVENTOR(S): Sidransky, David; Baylin, Stephen B.

PATENT ASSIGNEE(S): Johns Hopkins University School of Medicine, USA

SOURCE: PCT Int. Appl., 82 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent LANGUAGE: English

LANGUAGE: Englis
FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO.	KIND DATE	APPLICATION NO.	DATE
WO 9635704	A1 19961114	WO 1996-US6666	19960510
W: AU, CA,	CN, JP, KR		
RW: AT, BE,	CH, DE, DK, ES, FI,	FR, GB, GR, IE, IT	, LU, MC, NL,
PT, SE			
US 5767258	A 19980616	US 1995-439962	19950512
US 5856094	A 19990105	US 1995-497535	19950630
AU 9657399	A1 19961129	AU 1996-57399	19960510
PRIORITY APPLN. INFO	.:	US 1995-439962	19950512
		US 1995-497535	19950630
		WO 1996-US6666	19960510

AB Novel cell cycle regulatory polynucleotide transcripts and their encoded polypeptides are provided which were identified as the products of alternatively spliced mRNA for cyclin/CDK inhibitors, p16INK4A and p15INK4B, and a 5' nucleotide sequence referred to as 5'ALT. The p16 and p15 genes colocalize to human chromosome 9p21, which has been identified as a region having homozygous deletions in many tumors. 5'ALT also resides on chromosome 9p21, just 5' of exon 2 of p15, and about 30 kb upstream from p16. Polynucleotide transcripts are provided in which a 5'ALT polynucleotide is operatively linked to (1) exon 2 and exon 3 of p15 or (2) exon 2 of Searcher: Shears 308-4994

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p15. These transcripts are assocd. with normal growth control and regulation of cellular proliferation and provide a means for the development of more accurate diagnostic, prognostic, and therapeutic regimes for disorders assocd. with control of cell cycle progression and cell differentiation and the loss of such control. Methylation of p16 DNA and a resultant decrease in p16 gene expression is assocd. with transcriptional block and is assocd. with a variety of neoplasms. Thus, a method for detecting a neoplasm in a subject by detecting methylation of 5'CpG islands in p16 DNA, or detecting p16 mRNA or polypeptide levels in a sample is also provided. Preferably, the method utilizes a methylation-sensitive restriction endonuclease in order to detect p16 methylation. The 5'ALT, or 5'ALT-p16 or 5'ALT-p15 polypeptides can also be used to produce antibodies which are immunoreactive or bind to epitopes of the resp. polypeptides.

L3 ANSWER 6 OF 14 CAPLUS COPYRIGHT 1999 ACS

ACCESSION NUMBER: 1996:68700 CAPLUS

DOCUMENT NUMBER: 124:169878

TITLE: Difference in sero-diagnostic values among

KL-6-associated mucins classified as Cluster 9

AUTHOR(S): Kohno, Nobuoki; Inoue, Yoshikazu; Hamada,

Hironobu; Fujioka, Seiji; Fujino, Shun; Yokoyama, Akihito; Hiwada, Kunio; Ueda,

Norifumi; Akiyama, Mitoshi

CORPORATE SOURCE: School Medicine, Ehime University, Ehime,

791-02, Japan

SOURCE: Int. J. Cancer, Suppl. (1994), 8 (Third

International IASLC Workshop on Lung Tumor and

Differentiation Antigens, 1993), 81-3

CODEN: IJSUEZ; ISSN: 0898-6924

DOCUMENT TYPE: Journal

LANGUAGE: English

KL-6 classified as Cluster 9 (MUC-1) is a circulating high-mol.-wt. mucin-like mol. Serum level of KL-6 was measured by a sandwich assay using KL-6 antibody as not only a catcher but also as a tracer. The authors established 2 addnl. monoclonal antibodies (MAbs), LISA 101 and EH-123, reacting with KL-6 epitopes different from the epitope recognized by KL-6 antibody. The KL-6-assocd. mucins detected by the sandwich assay using LISA 101 or EH-123 antibody as a catcher and KL-6 antibody as a tracer were designated as LISA 1-6 and CAM 123-6 resp. The diagnostic values as the serum markers of KL-6, LISA 1-6 and CAM 123-6 were evaluated measuring their levels in the same serum from healthy individuals and from patients with pulmonary, pancreatic and breast adenocarcinomas. KL-6 was increased abnormally at high rates of more than 50% in pancreatic cancer and in benign lung diseases, LISA 1-6 only in pancreatic cancer, and CAM 123-6 only in pulmonary adenocarcinoma. In benign lung diseases, however, LISA 1-6 and CAM Searcher Shears

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123-6 were increased abnormally at the rates of only 5.3% and 0% resp. These observations clearly indicate that LISA 1-6 and CAM 123-6 constitute a part of KL-6, but that they are superior to KL-6 as tumor markers for pancreatic cancer and for pulmonary adenocarcinoma resp., because of their much lower false-pos. rates.

L3 ANSWER 7 OF 14 CAPLUS COPYRIGHT 1999 ACS ACCESSION NUMBER: 1994:104481 CAPLUS

DOCUMENT NUMBER: 120:104481

TITLE: Monoclonal antibodies against farmer's lung

antigens having specific binding to IgG

antibodies

AUTHOR(S): Kumar, Anoopa; Elms, Nancy; Kurup, Viswanath P.

CORPORATE SOURCE: Dep. Med., Med. Coll. Wisconsin, V., Milwaukee,

WI, USA

SOURCE: Int. Arch. Allergy Immunol. (1993), 102(1),

67-71

CODEN: IAAIEG; ISSN: 1018-2438

DOCUMENT TYPE: Journal LANGUAGE: English

Hypersensitivity pneumonitis resulting from environmental exposure to Saccharopolyspora rectivirgula (Micropolyspora faeni) among farmers has been well recognized. The diagnosis of the disease depends on demonstration of circulating antibodies against S. rectivirgula. However, dependable pure antigens are not available for serodiagnosis. The authors employed hybridoma technol. to obtain monoclonal antibodies against S. rectivirgula antigens. These monoclonal antibodies were employed to purify antigens through affinity chromatog. When tested in ELISA, high levels of antibodies were demonstrated against these antigens in farmer's lung patient sera compared to exposed but asymptomatic individuals from the same household. In Western blots, patient sera reacted with components of crude antigens with mol. masses of 28, 35, 60, 65 and 68 kD and 4 components above 100 kD, while the monoclonal antibodies reacted only with the 60-kD protein. These purified antigens can be used as reliable reagents in the specific diagnosis of farmer's lung diseases.

L3 ANSWER 8 OF 14 CAPLUS COPYRIGHT 1999 ACS ACCESSION NUMBER: 1993:467319 CAPLUS

DOCUMENT NUMBER: 119:67319

TITLE: Test reagent for hemoptysic sputum for

diagnosis of lung cancer

INVENTOR(S): Qin, Dexing

PATENT ASSIGNEE(S): Chinese Academy of Medical Sciences, Tumour

Hospital, Peop. Rep. China

SOURCE: Faming Zhuanli Shenqing Gongkai Shuomingshu, 4

pp.

CODEN: CNXXEV

DOCUMENT TYPE:

Patent

LANGUAGE:

Chinese

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE

CN 1069341

19930224 Α

CN 1991-105479 19910814

The title reagent contg. alc., H2O2, glacial AcOH, and AB guaiac gum is used for detecting hidden blood in sputum for alerting a possible lung cancer disease. Using the test reagent, the incidence of lung cancer was 40 times higher in pos.-responding people than in neg.-responding people.

ANSWER 9 OF 14 CAPLUS COPYRIGHT 1999 ACS

ACCESSION NUMBER:

1993:444470 CAPLUS

DOCUMENT NUMBER:

119:44470

TITLE:

Automated determination of crosslinked fibrin

derivatives in plasma

AUTHOR (S):

Elms, M. J.; Bundesen, P. G.; Rowbury, D.;

Goodall, S.; Wakeham. N.; Rowell, J. A.;

Hillyard, C. J.; Rylatt, D. B.

CORPORATE SOURCE:

Pathol. Dep., R. Brisbane Hosp., Brisbane,

Australia

SOURCE:

Blood Coagulation Fibrinolysis (1993), 4(1),

159-64

CODEN: BLFIE7; ISSN: 0957-5235

DOCUMENT TYPE:

LANGUAGE:

Journal English

Automated assays for the measurement of crosslinked fibrin derivs. in plasma (XL-FbDP) were developed by using latex beads coated with anti-D-dimer monoclonal antibody (DD-3B6/22) for both the Cobas Fara Chem. Centrifugal and the Cobas Mira analyzers (Roche, Basle, Switzerland). The analyzers were programmed to mix plasma and latex reagent simultaneously and analyze absorbance changes over a 10-15 min period. Results were interpolated by the analyzer from a std. curve derived from a polymer of D-dimer. Both assays had high precision (<5% CV) for values between 100 and 1000 ng/mL and provided clear discrimination between normal samples and samples from patients suffering from the thrombotic diseases deep vein thrombosis/pulmonary embolism and disseminated intravascular coagulation. The results obtained for XL-FbDP detn. with both methods compared well with established methods: a high correlation was obtained with a semiquant. manual latex method for both the Fara (r = 0.92) and Mira (r = 0.83) and correlations (r) of 0.81 (Fara) and 0.84 (Mira) were obtained with an EIA. Correlation between the 2 automated procedures was high (r = 0.96). The automated method will enable labs. to provide a rapid and accurate quantitation of Searcher Shears 308-4994 :

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XL-FbDP.

L3 ANSWER 10 OF 14 CAPLUS COPYRIGHT 1999 ACS

ACCESSION NUMBER:

1992:608482 CAPLUS

DOCUMENT NUMBER:

117:208482

TITLE:

Detection of early platelet activation and

prediagnosis of thrombotic events by immunoassay

for platelet surface thrombospondin (TSP)

INVENTOR(S):

Aiken, Martha L.; Painter, Richard G.

PATENT ASSIGNEE(S):

University of Texas System, USA

SOURCE:

PCT Int. Appl., 105 pp.

CODEN: PIXXD2
Patent

DOCUMENT TYPE: LANGUAGE:

English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PAT	ENT 1	10.		KI	ND :	DATE			AP	PLI	CATIO	ои ис	٥.	DATE		
	. -															
WO	92158	886		A:	1	1992	0917		WO	199	92 - US	S175	7	1992	0309	
	W:	AT,	AU,	BB,	BG,	BR,	CA,	CH,	CS,	DE,	DK,	ES,	FI,	GB,	HU,	JP,
		KP,	KR,	LK,	LU,	MG,	MN,	MW,	NL,	NO,	PL,	RO,	RU,	SD,	SE	
	RW:	ΑT,	BE,	BF,	ВJ,	CF,	CG,	CH,	CI,	CM,	DE,	DK,	ES,	FR,	GA,	GB,
		GN,	GR,	IT,	LU,	MC,	ML,	MR,	NL,	SE,	SN,	TD,	TG			
US	52565	538		Α		1993	1026		US	199	91-66	58272	2	1991	308	
AU	92165	554		A:	1	1992:	1006		AU	199	92-16	5554		1992	0309	
PRIORITY	APPI	LN.	INFO	. :					US	199	91-66	58272	2	1991	308	
									WO	199	92-US	31757	7	19920	309	

AB Persons at risk for a thrombotic event are identified by early immunol. detn. of elevated platelet surface TSP using a (labeled) monoclonal antibody to TSP. Thus, IgG-coated magnetic beads were exposed to an anti-TSP monoclonal antibody and then mixed with paraformaldehyde-fixed human platelets. After magnetic sepn. of the beads, the no. of platelets remaining in suspension was inversely related to TSP surface expression on the platelets. Diagnostic kits contg. reagents for the assay are described.

L3 ANSWER 11 OF 14 CAPLUS COPYRIGHT 1999 ACS

ACCESSION NUMBER:

1992:233421 CAPLUS

DOCUMENT NUMBER:

116:233421

TITLE:

Human surfactant protein-A contains blood group

A antigenic determinants

AUTHOR(S):

Stahlman, Mildred T.; Gray, Mary E.; Ross, Gary F.; Hull, William M.; Wikenheiser, Kathryn; Dingle, Sharon; Zelenski-Low, Kay R.; Whitsett,

Jeffrey A.

CORPORATE SOURCE:

Sch. Med., Vanderbilt Univ., Nashville, TN,

37232-2370, USA

SOURCE:

Pediatr. Res. (1992), 31(4, Pt. 1), 364-71

CODEN: PEREBL; ISSN: 0031-3998

DOCUMENT TYPE: Journal LANGUAGE: English

AB A major blood group antigenic epitope was identified on human pulmonary surfactant protein A (SP-A). Monoclonal (MAb) and polyclonal antibodies generated against purified human SP-A aggregated blood group A human erythrocytes and immunostained epithelial cells in a variety of human tissues, consistent with the tissue distribution of major blood group antigens. SP-A MAb (MAb-8) agglutinated red cells and immunostained tissues from A or AB blood groups, but did not react with cells or tissues from O or B individuals. MAb-8 immunostaining of tissue from blood group A individuals was ablated by incubation with blood group A red cells. MAb and polyclonal antibodies directed against A blood group antigens reacted strongly with purified SP-A obtained from a blood group A individual with alveolar proteinosis. MAb and polyclonal antibodies specific for B blood group antigen failed to react with SP-A from this patient or from patients who were in blood group B. Reactivity of anti-blood group MAb was lost after treatment of SP-A with endoglycosidase-F, demonstrating its reactivity with an epitope dependent on the asparagine-linked oligosaccharide at asparagine 187. Reactivity of MAb-8 with SP-A persisted after endoglycosidase-F treatment, but was lost after digestion with collagenase as assessed by Western blot after SDS-PAGE. Reactivity of MAb to SP-A was sensitive to .beta.-elimination, supporting the presence of another blood group antigenic site distinct from the epitope dependent on the asparagine-linked carbohydrate. The finding that the SP-A mol. contains a major blood group epitope has implication for the clin. use of surfactant replacement prepns. and diagnostic reagents based on this protein.

L3 ANSWER 12 OF 14 CAPLUS COPYRIGHT 1999 ACS ACCESSION NUMBER: 1989:210563 CAPLUS

DOCUMENT NUMBER: 110:210563

TITLE: Monoclonal antibodies to angiotensin-converting

enzyme: a powerful tool for lung and vessel

studies

AUTHOR(S): Danilov, S.; Sakharov, I.; Martynov, A.;

Faerman, A.; Muzykantov, V.; Klibanov, A.;

Trakht, I.

CORPORATE SOURCE: Inst. Exp. Cardiol., Cardiol. Res. Cent.,

Moscow, 121552, USSR

SOURCE: J. Mol. Cell. Cardiol. (1989), 21(Suppl. 1),

165-70

CODEN: JMCDAY; ISSN: 0022-2828

DOCUMENT TYPE: Journal LANGUAGE: English

AB A series (12 clones) of hybridomas were obtained, which produce

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monoclonal antibodies (Mab) to 5 different epitopes of the angiotensin-converting enzyme (ACE) mol. These antibodies may be used to (1) map antigenic structure of ACE, including the study of immunol. heterogeneity of ACE from different organs and tissues; (2) study the immunohistochem. distribution of ACE in human tissues, including the diagnosis of sarcoidosis; (3) develop an ACE immunoassay, and (4) prep. an immunosorbent for large-scale ACE isolation and for ACE-apheresis. One of the antibodies, 9B9, when injected into the circulation of rat and monkey, accumulated with high specificity in the lungs as compared with either normal mouse IgG or other organs and blood. The highly specific and nontoxic accumulation of Mab 9B9 suggests that it also may be used for .gamma. scintigraphy visualization of the pulmonary vascular bed, detection of lung injury, and as a vector for targeted drug delivery to the lung.

L3 ANSWER 13 OF 14 CAPLUS COPYRIGHT 1999 ACS

ACCESSION NUMBER: 1988:585013 CAPLUS

DOCUMENT NUMBER: 109:185013

TITLE: Diisocyanate antigens that detect specific

antibodies in exposed workers and guinea pigs

AUTHOR(S): Jin, Ruzhi; Karol, Meryl H.

CORPORATE SOURCE: Jilin Prov. Inst. Ind. Health Occup. Dis.,

Jilin, Peop. Rep. China

SOURCE: Chem. Res. Toxicol. (1988), 1(5), 288-93

CODEN: CRTOEC

DOCUMENT TYPE: Journal LANGUAGE: English

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Evaluation of the immunol. contribution to the pathogenesis of isocyanate lung disease necessitates prepn. of isocyanate-protein conjugates to detect anti-isocyanate antibodies. Sera were obtained from 2 guinea pigs immunized with MDI and from 3 workers with occupational exposure to MDI. By use of Western blot anal., guinea pig IgG antibodies were best detected by the monomeric component of MDI-guinea pig serum albumin. ELISA addnl. indicated that conjugates which contained a high d. of hapten detected greater amts. of antibody than did conjugates contg. low amts. of hapten. The same procedures were then used to assess the amt. of MDI-specific IgG and IgE antibody in sera from symptomatic workers. Effective MDI-HSA antigens were those that were monomeric and had high haptenic content. Highly substituted conjugates of monoisocyanates (Ph isocyanate and p-tolyl isocyanate) with serum albumins were also effective in detecting antibodies to MDI. These results indicate the importance of the compn. of isocyanate conjugate antigens in detecting antibodies to diisocyanates and suggest that stds. be developed for prepn. and characterization of these diagnostic serol. reagents.

ANSWER 14 OF 14 CAPLUS COPYRIGHT 1999 ACS

ACCESSION NUMBER: 1974:57087 CAPLUS

DOCUMENT NUMBER: 80:57087

TITLE: Modified procedure for evaluation of the

lecithin/sphingomyelin ratio in amniotic fluid

AUTHOR(S): Coch, Emily; Meyer, John S.; Goldman, Gordon;

Kessler, Gerald

CORPORATE SOURCE: Dep. Pathol. Lab. Med., Jew. Hosp., St. Louis,

Mo., USA

SOURCE: Clin. Chem. (1973), 19(9), 967-72

CODEN: CLCHAU

DOCUMENT TYPE: Journal LANGUAGE: English

Several modifications were made to the procedure of L. Gluck, et al. (1971) for evaluation of amniotic fluid lecithin/sphingomyelin (L/S) ratios. The acetone-pptn. step was eliminated, resulting in a faster extn. procedure and higher concns. of phospholipids. For faster thin-layer chromatog., silica gel-impregnated sheets of glass-fiber and a modified solvent system are used. For spot detection, a noncorrosive Bi subnitrate reagent specific for lecithin and sphingomyelin and an I vapor method to confirm the L/S ratio were used. The Bi spray also detected significant specimen contamination by phospholipids from plasma or erythrocytes. The L/S ratio was evaluated by visually comparing the relative size and color intensity of the lecithin and sphingomyelin TLC spots. An L/S ratio of 5 or more is consistent with mature pulmonary function and an L/S ratio of less than 2 suggests fetal pulmonary immaturity.

(FILE 'MEDLINE, BIOSIS, EMBASE, LIFESCI, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, PROMT, CANCERLIT' ENTERED AT 12:12:56 ON 25 OCT 1999)

L4 210 S L3

L5 113 DUP REM L4 (97 DUPLICATES REMOVED) L6 14 S L5 AND (HYBRIDIZ? OR HYBRIDIS?)

L6 ANSWER 1 OF 14 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD

ACCESSION NUMBER: 1999-418749 [35] WPIDS

CROSS REFERENCE: 1998-414099 [35]; 1998-414100 [35]; 1998-414105

[35]; 1998-414114 [35]; 1998-427559 [35];

1998-506364 [42]; 1998-520811 [44]; 1998-609887

[42]; 1999-059865 [05]; 1999-080881 [07];

1999-120770 [10]; 1999-132229 [11]; 1999-132234

[11]; 1999-204988 [17]; 1999-430031 [36]

DOC. NO. CPI: C1999-123038

TITLE: New isolated human genes encoding secreted

polypeptides.

DERWENT CLASS: B04 D16

INVENTOR(S): CARTER, K C; DUAN, R D; FENG, P; FERRIE, A M;

FLORENCE, C; FLORENCE, K; GREENE, J M; JANAT, F; KYAW, H; MOORE, P A; NI, J; ROSEN, C A; RUBEN, S M;

SHI, Y; SOPPET, D R; WEI, Y; YU, G

PATENT ASSIGNEE(S):

(HUMA-N) HUMAN GENOME SCI INC

COUNTRY COUNT:

82

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG

WO 9931117 A1 19990624 (199935)* EN 536

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW

W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZW

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE	
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WO 9931117	Α1	WO 1998-US27059	19981217	

PRIORITY APPLN. INFO: US 1997-68369 19971219; US 1997-68006 19971218; US 1997-68007 19971218; US 1997-68008 19971218; US 1997-68053 19971218; US 1997-68054 19971218; US 19971218; US 1997-68064 1997-68057 19971218; US 1997-70923 19971218; US 1997-68169 19971219; US 1997-68365 19971219; US 1997-68367 19971219; US 1997-68368 19971219

AN 1999-418749 [35] WPIDS

CR 1998-414099 [35]; 1998-414100 [35]; 1998-414105 [35]; 1998-414114 [35]; 1998-427559 [35]; 1998-506364 [42]; 1998-520811 [44]; 1998-609887 [42]; 1999-059865 [05]; 1999-080881 [07]; 1999-120770 [10]; 1999-132229 [11]; 1999-132234 [11]; 1999-204988 [17]; 1999-430031 [36]

AB WO 993111,7 A UPAB: 19990908

NOVELTY - Isolated human nucleic acids (I) encoding secreted proteins, are new.

DETAILED DESCRIPTION - (I) comprises a polynucleotide (PN) having a nucleotide sequence (NS) at least 95% identical to:

- (a) a PN fragment of one of a total of 110 defined human cDNA sequences given in the specification or a PN fragment of the cDNA sequence included in ATCC Deposit No. Z which is hybridizable to one of the 110 defined cDNA sequences;
- (b) a PN which is an (allelic) variant of one of the 110 defined cDNA sequences;
- (c) a PN encoding a biologically active polypeptide or a polypeptide fragment, domain or epitope of one of the 110 Searcher : Shears 308-4994

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defined amino acid sequences given in the specification or a polypeptide fragment, domain or epitope, respectively, encoded by a cDNA sequence included in ATCC Deposit No. Z which is hybridizable to one of the defined cDNA sequences;

- (d) a PN which encodes a species homolog of one of the 110 defined polypeptides; or
- (e) a PN capable of hybridizing under stringent conditions to any one of the PNs specified in (a)-(d), where the PN does not hybridize under stringent conditions to a sequence of only A residues or of only T residues.

ATCC Deposit No. Z refers to the representative clones, each containing a subset of the defined cDNA sequences, which have been deposited with the ATCC. The deposit numbers are ATCC 209463, 209511, 209551.

INDEPENDENT CLAIMS are also included for the following:

- (1) a recombinant vector comprising (I);
- (2) a method of making a recombinant host cell comprising (I);
- (3) a recombinant host cell produced by a method as in (2);
- (4) an isolated polypeptide comprising an amino acid sequence at least 95% identical to a polypeptide fragment (preferably having biological activity), domain, epitope, secreted form, full-length protein, (allelic) variant or species homologue of one of the 110 defined amino acid sequences or the encoded sequence included in ATCC Deposit No. Z;
- (5) an isolated antibody that binds specifically to an isolated polypeptide as in (4);
- (6) a recombinant host cell that expresses an isolated polypeptide as above;
- (7) a method of making an isolated polypeptide by culturing the host cell of (6);
 - (8) the polypeptide produced by the method of (7);
- (9) a gene corresponding to a cDNA sequence of the 110 defined amino acid sequences;
- (10) a method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:
- (a) determining the presence or absence of a mutation in (I); and
- (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or absence of the mutation;
- (11) a method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:
- (a) determining the presence or amount of expression of the polypeptide of (4) in a biological sample; and
- (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide;
- (12) a method for identifying a binding partner to the polypeptide of (4) comprising:

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- (a) contacting the polypeptide of (4) with a binding partner;
- (b) determining whether the binding partner effects an activity of the polypeptide; and
- (13) a method of identifying an activity in a biological assay, where the method comprises:
 - (a) expressing one of the 110 defined cDNAs in a cell;
 - (b) isolating the supernatant;
 - (c) detecting an activity in a biological assay; and
- (d) identifying the protein in the supernatant having the activity; and
 - (14) the product produced by the method of (13).

ACTIVITY - Cytostatic; Nootropic; Neuroprotective; Osteopathic; Antiseborreic; Dermatological; Antipsoritic; Antidiabetic; Antiasthmatic.

MECHANISM OF ACTION - None given.

USE - The PNs and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions (claimed), e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new PNs (claimed). Specific uses are described for each of the 110 PNs, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumors, neurodegenerative disorders, developmental abnormalities and fetal deficiencies, reproductive disorders, blood disorders, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, Alzheimer's and cognitive disorders, schizophrenia, disorders involving osteoclasts such as osteoporosis, arthritis, sepsis, acne, asthma, psoriasis, stroke, trauma, diseases of testes, lung or prostate, digestive/endocrine disorders, diabetes and AIDS. The polypeptides are also useful for identifying their binding partners (claimed). Dwg.0/0

L6 ANSWER 2 OF 14 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD

ACCESSION NUMBER: 1999-303069 [25] WPIDS

CROSS REFERENCE: 1999-312869 [25] DOC. NO. NON-CPI: N1999-227015

DOC. NO. CPI: N1999-227015
DOC. NO. CPI: C1999-089015

TITLE: New isolated human genes and the secreted

polypeptides they encode.

DERWENT CLASS: B04 D16 S03

INVENTOR(S): BREWER, L A; CARTER, K C; DUAN, D R; EBNER, R;

ENDRESS, G A; FENG, P; FLORENCE, C; FLORENCE, K A;

GREENE, J M; JANAT, F; KAYW, H; LAFLEUR, D W;

MOORE, P A; NI, J; OLSEN, H S; ROSEN, C A; RUBEN, S

M; SHI, Y; SOPPET, D R; WEI, Y; YOUNG, P

PATENT ASSIGNEE(S): (HUMA-N) HUMAN GENOME SCI INC.

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COUNTRY COUNT:

83

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG

WO 9922243 A1 19990506 (199925)* EN 546

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW

W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZW

AU 9912734 A 19990517 (199939)

APPLICATION DETAILS:

PATENT	NO	KIND	i	APPLICATION		DATE	
WO 992	 2243	Δ1		 WO	1998-US22376	19981023	
AU 991		A	i	ΑU	1999-12734	19981023	

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 9912734	A Based on	WO 9922243

PRIORITY APPLN. INFO: US 1997-63387 19971024; US 1997-62784

19971024; US 1997-63088 19971024; US 1997-63090
19971024; US 1997-63091 19971024; US 1997-63097
1997-63092 19971024; US 1997-63097
19971024; US 1997-63098 19971024; US 1997-63100
19971024; US 1997-63101 19971024; US 1997-63100
1997-63109 19971024; US 1997-63110
19971024; US 1997-63111 19971024; US

1997-63148 19971024; US 1997-63386 19971024

AN 1999-303069 [25] WPIDS

CR 1999-312869 [25]

AB WO 9922243 A UPAB: 19990707

NOVELTY - One hundred and forty eight isolated human genes and secreted proteins they encode are new.

DETAILED DESCRIPTION - An isolated nucleic acid molecule (NAM) (I) comprising a polynucleotide (PN) having a nucleotide sequence (NS) at least 95% identical to:

(a) a PN fragment of one of a total of 148 defined human cDNA sequences given in the specification or a PN fragment of the cDNA sequence included in ATCC Deposit No. Z which is

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hybridisable to one of the 148 defined cDNA sequence;

- (b) a PN which is an (allelic) variant of one of the 148 defined cDNA sequences;
- (c) a PN encoding a biologically active polypeptide or a polypeptide fragment, domain or epitope of one of the 148 defined amino acid sequences given in the specification or a polypeptide fragment encoded by a cDNA sequence included in ATCC Deposit No. Z which is hybridisable to one of the defined cDNA sequences;
- (d) a PN which encodes a species homologue of one of the 148 defined polypeptides; or
- (e) a PN capable of **hybridising** under stringent conditions to any one of the PNs specified in (a)-(d), where the PN does not **hybridise** under stringent conditions to a sequence of only A residues or of only T residues.

INDEPENDENT CLAIMS are also included for:

- (1) a recombinant vector comprising (I);
- (2) a method of making a recombinant host cell comprising (I);
- (3) a recombinant host cell produced by a method as in (2);
- (4) an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from a polypeptide fragment (preferably having biological activity), domain, epitope, secreted form, full-length protein, (allelic) variant or species homologue of one of the 148 defined amino acid sequences or the encoded sequence included in ATCC Deposit No. Z;
- (5) an isolated antibody that binds specifically to an isolated polypeptide as in (4); and
- (6) a recombinant host cell that expresses a gene corresponding to a cDNA sequence of the 148 defined amino acid sequences.

Note: From the disclosure 'ATCC Deposit No. Z' refers to the representative clones, each containing a subset of the defined cDNA sequences, which have been deposited with the ATCC. The deposit numbers are: ATCC 209299, 209346, 209300, 209324.an isolated polypeptide as above;

ACTIVITY - None given.

MECHANISM OF ACTION - None given.

USE - The PNs and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions (claimed), e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new PNs (claimed). Specific uses are described for each of the 148 PNs, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and fetal deficiencies, blood disorders, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, ischemic shock, Alzheimer's and cognitive Searcher: Shears 308-4994

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disorders, schizophrenia, prostate diseases, obesity, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, **diseases** of testes, **lung** or thymus, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for **identifying** their binding partners (claimed).

L6 ANSWER 3 OF 14 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD

ACCESSION NUMBER:

1999-167452 [14] WPIDS

DOC. NO. CPI:

C1999-048990

TITLE:

New isolated human genes encoding secreted

polypeptides - useful for diagnosis and treatment

of pathalogical diseases.

DERWENT CLASS:

B04 D16

INVENTOR(S):

BREWER, L A; EBNER, R; FERRIE, A M; GREENE, J M;

JANAT, F; NI, J; OLSEN, H S; ROSEN, C A; RUBEN, S

M; SOPPET, D R; YOUNG, P E; YU, G

PATENT ASSIGNEE(S):

(HUMA-N) HUMAN GENOME SCI INC

COUNTRY COUNT:

82

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG

WO 9907891 A1 19990218 (199914)* EN 329

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC

MW NL OA PT SD SE SZ UG ZW

W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI

GB GE GH GM HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT

LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL

TJ TM TR TT UA UG US UZ VN YU ZW

AU 9887684 A 19990301 (199928)

APPLICATION DETAILS:

IMIDNI NO	KIND	APPLICATION	DATE
WO 9907891	A1	WO 1998-US16235	
AU 9887684	A	AU 1998-87684	19980804

FILING DETAILS:

PATENT NO	KIND	PATENT NO

AU 9887684 A Based on

WO 9907891

PRIORITY APPLN. INFO: US 1997-56732 19970819; US 1997-54798

19970805; US 1997-54803 19970805; US 1997-54806 19970805; US 1997-54807 19970805; US

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1997-54808 19970805; US 1997-54809 19970805; US 1997-55309 19970805; US 1997-55310 19970805; US 1997-55311 19970805; US 1997-55312 19970805; US 1997-55386 19970805; US 1997-55970 19970818; US 1997-55986 19970818; US 1997-56364 19970819; US 1997-56365 19970819; US 1997-56366 19970819; US 19970819; US 1997-56370 1997-56367 19970819; US 1997-56371 19970819; US 1997-56557 19970819; US 1997-56563 19970819; US 1997-56731

ΔN 1999-167452 [14] WPTDS AB

9907891 A UPAB: 19990412

NOVELTY - A total of 90 new isolated human genes encode secreted polypeptides which can be used in the diagnosis and treatment of pathalogical diseases such as cancers, neurological disorders, immune diseases, inflammation or blood disorders.

DETAILED DESCRIPTION - IDEPENDENT CLAIMS are included for the following: (1) An isolated nucleic acid molecule (NAM) (I) is claimed comprising a polynucleotide (PN) having a nucleotide sequence (NS) at least 95% identical to: (a) a PN fragment of one of a total of 90 defined human cDNA sequences given in the specification or a PN fragment of the cDNA sequence included in ATCC Deposit No. Z which is hybridisable to one of the 90 defined cDNA sequence; (b) a PN which is an (allelic) variant of one of the 90 defined cDNA sequences; (c) a PN encoding a biologically active polypeptide or a polypeptide fragment, domain or epitope of one of the 90 defined amino acid sequences given in the specification or a polypeptide fragment encoded by a cDNA sequence included in ATCC Deposit No. Z which is hybridisable to one of the defined cDNA sequences; (d) a PN which encodes a species homologue of one of the 90 defined polypeptides; or (e) a PN capable of hybridising under stringent conditions to any one of the PNs specified in (a)-(d), where the PN does not hybridise under stringent conditions to a sequence of only A residues or of only T residues; (2) a recombinant vector comprising (I); (3) a method of making a recombinant host cell comprising (I); (4) a recombinant host cell produced by a method as in (3); (5) an isolated polypeptide comprising an amino acid sequence homologous to a sequence selected from a polypeptide fragment (preferably having biological activity), domain, epitope, secreted form, full-length protein, (allelic) variant or species homologue of one of the 90 defined amino acid sequences or the encoded sequence included in ATCC Deposit No. Z; (6) an isolated antibody that binds specifically to an isolated polypeptide as in (5); (7) a recombinant host cell that expresses an isolated polypeptide as above; and (8) a gene corresponding to a cDNA sequence of the 90 defined amino acid Searcher Shears

		19	

sequences. Note: From the disclosure 'ATCC Deposit No. Z' refers to the representative clones, each containing a subset of the defined cDNA sequences, which have been deposited with the ATCC. The deposit numbers are: ATCC 209146, 209177, 209179 and 209180.

USE - The PNs and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions (claimed), e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new PNs (claimed). Specific uses are described for each of the 90 PNs, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, CNS disorders, diseases of the immune system, autoimmune diseases, hepatic and renal disease, diabetes, inflammation, allergies, ischemic shock, Alzheimer's and cognitive disorders, schizophrenia, cardiovascular disorders, prostate diseases, asthma, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, diseases of testes, lung or thymus, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners (claimed). Dwq.0/0

L6 ANSWER 4 OF 14 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD

ACCESSION NUMBER:

1999-153691 [13] WPIDS

DOC. NO. CPI:

C1999-045418

TITLE:

New isolated human genes and the secreted

polypeptides they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.

DERWENT CLASS:

B04 D16

82

INVENTOR (S):

CARTER, K C; ENDRESS, G A; FAN, P; FENG, P; KYAW, H; LAFLEUR, D W; LI, Y; MOORE, P A; ROSEN, C A;

RUBEN, S M; SHI, Y; WEI, Y; ZENG, Z

PATENT ASSIGNEE(S):

(HUMA-N) HUMAN GENOME SCI INC

COUNTRY COUNT:

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG

WO 9906423 A1 19990211 (199913)* EN 311

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW

W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI
GB GE GH GM HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT
LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL
TJ TM TR TT UA UG US UZ VN YU ZW

AU 9887634 A 19990222 (199927)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9906423	A1	WO 1998-US15949	19980729
AII 9887634	A	AU 1998-87634	19980729

FILING DETAILS:

AB

PATENT NO	KIND			PAT	TENT NO
			-	- - - -	
AU 9887634	Α	Based	on	WO	9906423

19970819; US 1997-54209 PRIORITY APPLN. INFO: US 1997-56730 19970730; US 1997-54211 19970730; US 19970730; US 1997-54213 1997-54212 19970730; US 19970730; US 1997-54214 19970730; US 1997-54217 1997-54215 19970730; US 1997-54218 19970730; US 19970730; US 1997-54236 1997-54234 19970818; US 19970730; US 1997-55968 19970818; US 1997-55972 1997-55969 19970819; US 19970818; US 1997-56534 19970819; US 1997-56554 1997-56543 19970819; US 1997-56561 19970819; US 19970819 19970819; US 1997-56729 1997-56727

AN 1999-153691 [13] WPIDS

WO 9906423 A UPAB: 19990331

An isolated nucleic acid molecule (NAM) (I) is claimed comprising a polynucleotide (PN) having a nucleotide sequence (NS) at least 95% identical to: (a) a PN fragment of one of a total of 83 defined human cDNA sequences given in the specification or a PN fragment of the cDNA sequence included in ATCC Deposit No. Z which is hybridisable to one of the 83 defined cDNA sequence; (b) a PN which is an (allelic) variant of one of the 83 defined cDNA sequences; (c) a PN encoding a biologically active polypeptide or a polypeptide fragment, domain or epitope of one of the 83 defined amino acid sequences given in the specification or a polypeptide fragment encoded by a cDNA sequence included in ATCC Deposit No. Z which is hybridisable to one of the defined cDNA sequences; (d) a PN which encodes a species homologue of one of the 83 defined polypeptides; or (e) a PN capable of hybridising under stringent conditions to any one of the PNs specified in (a)-(d), where the PN does not hybridise under stringent conditions to a sequence of only A residues or of only T residues. Also claimed are: (1) a recombinant vector comprising (I); (2) a method of making a recombinant host cell Shears 308-4994 Searcher

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comprising (I); (3) a recombinant host cell produced by a method as in (2); (4) an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from a polypeptide fragment (preferably having biological activity), domain, epitope, secreted form, full-length protein, (allelic) variant or species homologue of one of the 83 defined amino acid sequences or the encoded sequence included in ATCC Deposit No. Z; (5) an isolated antibody that binds specifically to an isolated polypeptide as in (4); (6) a recombinant host cell that expresses an isolated polypeptide as above; and (7) a gene corresponding to a cDNA sequence of the 83 defined amino acid sequences. Note: From the disclosure ATCC Deposit No. Z refers to the representative clones, each containing a subset of the defined cDNA sequences, which have been deposited with the ATCC. The deposit numbers are: ATCC 209145, 209148, 209147.

USE- The PNs and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions (claimed), e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new PNs (claimed). Specific uses are described for each of the 83 PNs, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, ischemic shock, Alzheimer's and cognitive disorders, schizophrenia, restenosis, prostate diseases, obesity, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, diseases of lung or skin, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners (claimed). Dwg.0/0

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DERWENT INFORMATION LTD
    ANSWER 5 OF 14 WPIDS COPYRIGHT 1999
                     1999-120770 [10] WPIDS
ACCESSION NUMBER:
                     1998-414099 [35]; 1998-414100 [35]; 1998-414105
CROSS REFERENCE:
                     [35]; 1998-414114 [35]; 1998-427559 [35];
                     1998-506364 [42]; 1998-520811 [44]; 1998-609887
                      [42]; 1999-059865 [05]; 1999-080881 [07];
                     1999-132229 [11]; 1999-132234 [11]; 1999-204988
                      [17]; 1999-418749 [32]; 1999-430031 [36]
                     C1999-035369
DOC. NO. CPI:
                     New isolated human genes and the secreted
TITLE:
                     polypeptides they encode - useful for diagnosis and
                      treatment of e.g. cancers, neurological disorders,
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Searcher :

immune diseases, inflammation or blood disorders.

Shears 308-4994

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DERWENT CLASS:

B04 D16

INVENTOR(S):

BREWER, L A; EBNER, R; FISCHER, C L; KYAW, H;

LAFLEUR, D W; LI, Y; MOORE, P A; OLSEN, H S; ROSEN,

C A; RUBEN, S M; SHI, Y; SOPPET, D R; ZENG, Z

PATENT ASSIGNEE(S): (HUMA-N) HUMAN GENOME SCI INC

COUNTRY COUNT:

83

PATENT INFORMATION:

PATENT N	O KIND	DATE	WEEK	LA	PG

WO 9902546 A1 19990121 (199910)* EN 462

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC

MW NL OA PT SD SE SZ UG ZW

W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM GW HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS

LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK

SL TJ TM TR TT UA UG US UZ VN YU ZW

AU 9884743 A 19990208 (199924)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9902546	A1	WO 1998-US13684	19980707
AII 9884743	A	AU 1998-84743	19980707

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 9884743	A Based on	WO 9902546

PRIORITY APPLN. INFO: US 1997-58785 19970912; US 1997-51916 19970708; US 1997-51918 19970708; US 1997-51919 19970708; US 1997-51920 19970708; US 1997-51925 19970708; US 19970708; US 1997-51928 1997-51926 19970708; US 1997-51929 19970708; US 1997-51930 19970708; US 1997-51931 19970708; US 1997-51932 19970708; US 19970708; US 1997-52733 1997-52732 19970708; US 1997-52793 19970708; US 19970708; US 1997-52803 1997-52795 19970818; US 19970708; US 1997-55684 19970818; US 1997-55723 1997-55722 19970818; US 1997-55947 19970818; US 1997-55948 19970818; US 1997-55949 19970818; US 1997-55950 19970818; US 1997-55953 19970818; US 1997-55954 Searcher: Shears 308-4994

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19970818; US 1997-55964 19970818; US 1997-55984 19970818; US 1997-56360 19970818; US 1997-58660 19970912; US 1997-58661 19970912; US 1997-58664 19970912 WPIDS ΝA 1999-120770 [10] 1998-414099 [35]; 1998-414100 [35]; 1998-414105 [35]; 1998-414114 CR [35]; 1998-427559 [35]; 1998-506364 [42]; 1998-520811 [44]; 1998-609887 [42]; 1999-059865 [05]; 1999-080881 [07]; 1999-132229 [11]; 1999-132234 [11]; 1999-204988 [17]; 1999-418749 [32]; 1999-430031 [36] 9902546 A UPAB: 19990908 AB An isolated nucleic acid molecule (NAM) (I) is claimed comprising a polynucleotide (PN) having a nucleotide sequence (NS) at least 95% identical to: (a) a PN fragment of one of a total of 123 defined human cDNA sequences given in the specification or a PN fragment of the cDNA sequence included in ATCC Deposit No. Z which is hybridisable to one of the 123 defined cDNA sequence; (b) a PN which is an (allelic) variant of one of the 123 defined cDNA sequences; (c) a PN encoding a biologically active polypeptide or a polypeptide fragment, domain or epitope of one of the 123 defined amino acid sequences given in the specification or a polypeptide fragment encoded by a cDNA sequence included in ATCC Deposit No. Z which is hybridisable to one of the defined cDNA sequences; (d) a PN which encodes a species homologue of one of the 123 defined polypeptides; or (e) a PN capable of hybridising under stringent conditions to any one of the PNs specified in (a)-(d), where the PN does not hybridise under stringent conditions to a sequence of only A residues or of only T residues. Also claimed are: (1) a recombinant vector comprising (I); (2) a method of making a recombinant host cell comprising (I); (3) a recombinant host cell produced by a method as in (2); (4) an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from a polypeptide fragment (preferably having biological activity), domain, epitope, secreted form, full-length protein, (allelic) variant or species homologue of one of the 123 defined amino acid sequences or the encoded sequence included in ATCC Deposit No. Z; (5) an isolated antibody that binds specifically to an isolated polypeptide as in (4); (6) a recombinant host cell that expresses an isolated polypeptide as above; and (7) a gene corresponding to a cDNA sequence of the 123 defined amino acid sequences. Note: From the disclosure 'ATCC Deposit No. Z' refers to the representative clones, each containing a subset of the defined cDNA sequences, which have been deposited with the ATCC. deposit numbers are: ATCC 209119, 209124, 209125, 209126. USE - The PNs and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions

(claimed), e.g. by protein or gene therapy. Also pathological

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conditions can be diagnosed by determining the

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amount of the new polypeptides in a sample or by determining the presence of mutations in the new PNs (claimed). Specific uses are described for each of the 123 PNs, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, ischemic shock, Alzheimer's and cognitive disorders, schizophrenia, restenosis, prostate diseases, obesity, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, diseases of testes, lung or thyroid, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding

polypeptides are also useful for **identifying** their binding partners (claimed).

Dwg.0/0

L6 ANSWER 6 OF 14 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD

ACCESSION NUMBER:

1999-070066 [06] WPIDS

DOC. NO. CPI:

C1999-020600

TITLE:

New isolated human genes and the secreted

polypeptides they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.

DERWENT CLASS:

B04 D16

INVENTOR(S):

BREWER, L A; DUAN, R; EBNER, R; FERRIE, A M; FLORENCE, K A; GREENE, J M; HU, J; LAFLEUR, D W; MOORE, P A; NI, J; OLSEN, H S; ROSEN, C A; RUBEN, S

M; SHI, Y; YOUNG, P

PATENT ASSIGNEE(S):

(HUMA-N) HUMAN GENOME SCI INC

COUNTRY COUNT:

81

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG

WO 9842738 A1 19981001 (199906) * EN 385

RW: AT BE CH DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW

W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI
GB GE GH GM GW HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT
LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL
TJ TM TR TT UA UG US UZ VN YU ZW

AU 9865646 A 19981020 (199909)

APPLICATION DETAILS:

AU 9865646 A

AU 1998-65646 19980319

FILING DETAILS:

PATENT NO KIND

PATENT NO

AU 9865646

A Based on

WO 9842738

PRIORITY APPLN. INFO: US 1997-50937 19970530; US 1997-41276 19970321; US 1997-41277 19970321; US 1997-41281 19970321; US 1997-42344 19970321; US 1997-48069 19970530; US 1997-48094 19970530; US 1997-48095 19970530; US 1997-48096 19970530; US 1997-48099 19970530; US 1997-48131 19970530; US 1997-48135 19970530; US 1997-48154 19970530; US 1997-48160 19970530; US 1997-48186 19970530; US 1997-48187 19970530; US 1997-48188 19970530; US 1997-48351 19970530; US 1997-48352 19970530; US 1997-48355 19970530

AN 1999-070066 [06] WPIDS

AB WO 9842738 A UPAB: 19990210

An isolated nucleic acid molecule (NAM) (I) comprises a polynucleotide (PN) having a nucleotide sequence (NS) at least 95% identical to:(a) a PN fragment of one of a total of 87 defined human cDNA sequences given in the specification or a PN fragment of the cDNA sequence included in ATCC Deposit No. Z which is hybridisable to one of the 87 defined cDNA sequences; (b) a PN which is an (allelic) variant of one of the 87 defined cDNA sequences; (c) a PN encoding a biologically active polypeptide or a polypeptide fragment, domain or epitope of one of the 87 defined amino acid sequences given in the specification or a polypeptide fragment encoded by a cDNA sequence included in ATCC Deposit No. Z which is hybridisable to one of the defined cDNA sequence; (d) a PN which encodes a species homologue of one of the 87 defined polypeptides; or (e) a PN capable of hybridising under stringent conditions to any one of the PNs specified in (a)-(d), where the PN does not hybridise under stringent conditions to a sequence of only A residues or of only T residues. Also claimed are: (1) a recombinant vector comprising (I); (2) a method of making a recombinant host cell comprising (I); (3) a recombinant host cell produced by a method as in (2); (4) an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from a polypeptide fragment (preferably having biological activity), domain, epitope, secreted form, full-length protein, (allelic) variant or species homologue of one of the 87 defined amino acid sequences or the encoded sequence included in ATCC Searcher Shears 308-4994

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Deposit No. Z; (5) an isolated antibody that binds specifically to an isolated polypeptide as in (4); (6) a recombinant host cell that expresses an isolated polypeptide as in (4); and (7) a gene corresponding to a cDNA sequence of the 87 defined amino acid sequences. Note: From the disclosure 'ATCC Deposit No. Z' refers to the representative clones, each containing a subset of the defined cDNA sequences, which have been deposited with the ATCC. The deposit numbers are: ATCC 97923, 97924, 97957, 97958, 209071, 209641, 209072 and 209073.

USE - The PNs and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions (claimed), e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new PNs (claimed). Specific uses are described for each of the 87 PNs, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukaemias, diseases of the immune system (including allergies or asthma), lymphocytic diseases, brain associated diseases, hepatic and renal disease, lymphomas, inflammation, ischemic shock, Alzheimer's and cognitive disorders, schizophrenia, restenosis, prostate diseases, obesity, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, diseases of testis, lung or thymus, digestive/endocrine disorders, including metabolic regulation, malabsorption, gastritis and neoplasms, and AIDS. The polypeptides are also useful for identifying their binding partners (claimed). Dwg.0/0

ANSWER 7 OF 14 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD L6

1999-060335 [05] WPIDS ACCESSION NUMBER:

N1999-044750 DOC. NO. NON-CPI: C1999-018022 DOC. NO. CPI:

New LS170 nucleic acid from lung tissue - useful TITLE:

for detecting, monitoring, preventing and

treating lung disease,

particularly cancer.

DERWENT CLASS:

B04 D16 S03

INVENTOR (S):

BILLING-MEDEL, P A; COHEN, M; COLPITTS, T L; FRIEDMAN, P N; GORDON, J; GRANADOS, E N; HODGES, S C: KLASS, M R; KRATOCHVIL, J D; ROBERTS-RAPP, L;

RUSSELL, J C; STROUPE, S D

PATENT ASSIGNEE(S):

(ABBO) ABBOTT LAB

COUNTRY COUNT:

20

PATENT INFORMATION:

Shears 308-4994 Searcher :

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PATENT NO KIND DATE WEEK LA PG

WO 9856951 A1 19981217 (199905) * EN 119

RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE W: CA JP

APPLICATION DETAILS:

PRIORITY APPLN. INFO: US 1997-49183 19970611

AN 1999-060335 [05] WPIDS

AB WO 9856951 A UPAB: 19990210

Detection of a target LS170 polynucleotide (I) comprises treating a test sample with at least one LS170-specific nucleic acid (II) that has at least 50% identify with any of 9 sequences ((1)-(9), reproduced, of 251, 243, 258, 202, 458, 273, 200,1009 and 1027 bp, respectively), their fragments or complements. Also new are (a) LS170 sequences, or their fragments, that hybridise selectively to the LS170 gene and have at least 50% identity with (i) (1)-(9), other than (5) or their complements, or (ii) fragments of (1)-(7); (b) recombinant expression system containing (II) plus a control sequence; (c) cells transformed with this expression system; (d) LS170 polypeptides (III) at least 50% identical with 9 sequences ((23)-(31), of 256, 18, 26, 29, 12, 15, 11 or 19 amino acids (aa), reproduced), or their fragments, containing at least one LS170 epitope; (e) antibodies (Ab) specific for at least one LS170 epitope present on (III); (f) cells transformed with any of (1)-(9), their fragments or complements, encoding at least one epitope of LS170; (g) (I) having at least 50% identity with (i) any of (1)-(9), their fragments or complements or (ii) fragments of (1)-(7); (h) genes, or their fragments, encoding LS170 proteins at least 50% identical with (23); (j) genes, or their fragments, at least 50% identical with (8) or (9).

USE - LS170 represents a set of contiguous, partially overlapping sequences transcribed from lung tissue. They are used for diagnosis, staging, monitoring, in vivo imaging, prevention and treatment of lung disease, specifically cancer, and to indicate predisposition to such disease. Particularly detection of (I), LS170 antigens (using Ab in immunoassays) or anti-LS170 antibodies (using LS170 as antigen) is indicative of disease. Cells of (c) are used to express recombinant (III), used to raise Ab and for drug screening. LS170-related nucleic acid can be used to isolate related sequences; as standards and reagents in assays; as targets for drug screening, and as components or targets for therapy, e.g. as antisense, ribozyme or Searcher: Shears 308-4994

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triplex-forming agents. Ab can be used to deliver therapeutic agents to LS170-expressing cells; directly as therapeutic agents (by neutralising LS170 polypeptides); in competitive binding drug screens, and to generate anti-idiotypic antibodies for use in rational drug design.

Dwg.0/4

L6 ANSWER 8 OF 14 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD

ACCESSION NUMBER: 1999-059865 [05] WPIDS

CROSS REFERENCE: 1998-414099 [35]; 1998-414100 [35]; 1998-414105

[35]; 1998-414114 [35]; 1998-427559 [35];

1998-506364 [42]; 1998-520811 [44]; 1998-609887

[42]; 1999-080881 [07]; 1999-120770 [10];

1999-132229 [11]; 1999-132234 [11]; 1999-204988

[17]; 1999-418749 [32]; 1999-430031 [36]

DOC. NO. NON-CPI: N1999-044486 DOC. NO. CPI: C1999-017701

TITLE: New isolated human genes and the secreted

polypeptides they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.

DERWENT CLASS: B04 D16 S03

INVENTOR(S): BREWER, L A; CARTER, K C; DILLON, P J; EBNER, R;

ENDRESS, G A; FAN, P; FENG, P; FERRIE, A M; FISCHER, C L; FLORENCE, C; FLORENCE, K; GREENE, J M; HU, J; KYAW, H; LAFLEUR, D W; LI, Y; MOORE, P A;

NI, J; OLSEN, H S; ROSEN, C A; RUBEN, S M; SHI, Y;

SOPPET, D R; WEI, Y; YOUNG, P; YU, G; ZENG, Z

PATENT ASSIGNEE(S): (HUMA-N) HUMAN GENOME SCI INC

COUNTRY COUNT: 82

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG

WO 9854963 A2 19981210 (199905)* EN 770

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW

W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI
GB GE GH GM GW HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT
LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL
TJ TM TR TT UA UG US UZ VN YU ZW

AU 9878120 A 19981221 (199919)

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 9854963	A2		WO 1998-US11	422 19980604
AU 9878120	A		AU 1998-7812	0 19980604
		Searcher	· Shears	308-4994

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FILING DETAILS:

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PATENT NO KIND
                                    PATENT NO
    ______
    AU 9878120 A Based on
                                    WO 9854963
PRIORITY APPLN. INFO: US 1997-70923
                                   19971218; US 1997-48875
                    19970606; US 1997-48876 19970606; US
                    1997-48877 19970606; US 1997-48878
                    19970606; US 1997-48880
                                             19970606; US
                    1997-48881
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                                 19970606; US 1997-48885
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                    1997-48893
                                 19970606; US 1997-48894
                    19970606; US 1997-48895
                                             19970606; US
                                19970606; US 1997-48897
                    1997-48896
                    19970606; US 1997-48898
                                             19970606; US
                    1997-48899 19970606; US 1997-48900
                    19970606; US 1997-48901 19970606; US
                    1997-48915
                                19970606; US 1997-48916
                    19970606; US 1997-48917
                                            19970606; US
                                19970606; US 1997-48962
                    1997-48949
                    19970606; US 1997-48963
                                             19970606; US
                    1997-48964
                                 19970606; US 1997-48970
                    19970606; US 1997-48971
                                             19970606; US
                                19970606; US 1997-48974
                    1997-48972
                    19970606; US 1997-49019 19970606; US
                    1997-49020
                                19970606; US 1997-49373
                    19970606; US 1997-49374 19970606; US
                                 19970606; US 1997-57584
                    1997-49375
                    19970905; US 1997-57627
                                             19970905; US
                                19970905; US 1997-57629
                    1997-57628
                    19970905; US 1997-57634 19970905; US
                                19970905; US 1997-57642
                    1997-57635
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                                             19970905; US
                                 19970905; US 1997-57645
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                    19970905; US 1997-57654
                                            19970905; US
                    1997-57661
                                19970905; US 1997-57662
                    19970905; US 1997-57666 19970905; US
                                19970905; US 1997-57668
                    1997-57667
                    19970905; US 1997-57760
                                             19970905; US
                    1997-57761 19970905; US 1997-57762
                    19970905; US 1997-57763 19970905; US
                          Searcher: Shears 308-4994
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1997-57764 19970905; US 1997-57765 19970905; US 1997-57769 19970905; US 1997-57770 19970905; US 1997-57771 19970905; US 1997-57774 19970905; US 1997-57775 19970905; US 1997-57776 19970905; US 1997-57777 19970905; US 1997-57778 19970905

AN 1999-059865 [05] WPIDS
CR 1998-414099 [35]; 1998-414100 [35]; 1998-414105 [35]; 1998-414114 [35]; 1998-427559 [35]; 1998-506364 [42]; 1998-520811 [44]; 1998-609887 [42]; 1999-080881 [07]; 1999-120770 [10]; 1999-132229 [11]; 1999-132234 [11]; 1999-204988 [17]; 1999-418749 [32]; 1999-430031 [36]

AB

sequences.

9854963 A UPAB: 19990908 WO An isolated nucleic acid molecule (NAM) (I) comprising a polynucleotide (PN) having a nucleotide sequence (NS) at least 95% identical to: (a) a PN fragment of one of a total of 207 defined human cDNA sequences given in the specification or a PN fragment of the cDNA sequence included in ATCC Deposit No. Z which is hybridisable to one of the 207 defined cDNA sequence; (b) a PN which is an (allelic) variant of one of the 207 defined cDNA sequences; (c) a PN encoding a biologically active polypeptide or a polypeptide fragment, domain or epitope of one of the 207 defined amino acid sequences given in the specification or a polypeptide fragment encoded by a cDNA sequence included in ATCC Deposit No. Z which is hybridisable to one of the defined cDNA sequences; (d) a PN which encodes a species homologue of one of the 207 defined polypeptides; or (e) a PN capable of hybridising under stringent conditions to any one of the PNs specified in (a)-(d), where the PN does not hybridise under stringent conditions to a sequence of only A residues or of only T residues. Also claimed are: (1) a recombinant vector comprising (I); (2) a method of making a recombinant host cell comprising (I); (3) a recombinant host cell produced by a method as in (2); (4) an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from a polypeptide fragment (preferably having biological activity), domain, epitope, secreted form, full-length protein, (allelic) variant or species homologue of one of the 207 defined amino acid sequences or the encoded sequence included in ATCC Deposit No. Z; (5) an isolated antibody that binds specifically to an isolated polypeptide as in (4); (6) a recombinant host cell that expresses an isolated polypeptide as above; and (7) a gene

Note: From the disclosure 'ATCC Deposit No. Z' refers to the representative clones, each containing a subset of the defined cDNA sequences, which have been deposited with the ATCC. The deposit numbers are: ATCC 97979, 97974, 97975, 97976, 97977, 209007, 209008, Searcher: Shears 308-4994

corresponding to a cDNA sequence of the 207 defined amino acid

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		*)	

209009, 209010, 209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511,

USE The PNs and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions (claimed), e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new PNs (claimed). Specific uses are described for each of the 207 PNs, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, ischemic shock, Alzheimer's and cognitive disorders, schizophrenia, restenosis, prostate diseases, obesity, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, diseases of testes, lung or thymus, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners (claimed). Dwq.0/0

DERWENT INFORMATION LTD ANSWER 9 OF 14 WPIDS COPYRIGHT 1999 L6

ACCESSION NUMBER:

WPIDS 1998-609887

CROSS REFERENCE:

1998-414099 [35]; 1998-414100 [35]; 1998-414105

[35]; 1998-414114 [35]; 1998-427559 [35];

1998-506364 [42]; 1998-520811 [44]; 1999-059865

[05]; 1999-080881 [07]; 1999-120770 [10];

1999-132229 [11]; 1999-132234 [11]; 1999-204988

[17]; 1999-418749 [32]; 1999-430031 [36]

DOC. NO. NON-CPI:

DOC. NO. CPI:

N1998-474475 C1998-182720

TITLE:

New isolated human genes and the secreted

polypeptides they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders,

immune diseases, inflammation or blood disorders.

DERWENT CLASS:

INVENTOR (S):

B04 D16 S03

BEDNARIK, D P; BREWER, L A; CARTER, K C; DUAN, R; EBNER, R; ENDRESS, G A; FENG, P; FERRIE, A M; FISCHER, C L; FLORENCE, K A; GREENE, J M; HU, J; NI, J; OLSEN, H S; ROSEN, C A; RUBEN, S M; SOPPET, D R; YOUNG, P E; YU, G; KYAW, H; LAFLEUR, D W; LI,

Y: MOORE, PA; SHI, Y; ZENG, Z

PATENT ASSIGNEE(S):

(HUMA-N) HUMAN GENOME SCI INC

COUNTRY COUNT:

81

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LΑ PG

> Shears 308-4994 Searcher

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WO 9839446 A2 19980911 (199851)* EN 447

RW: AT BE CH DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW

NL OA PT SD SE SZ UG ZW

AU 9865452 A 19980922 (199908)

W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM GW HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL

TJ TM TR TT UA UG US UZ VN YU ZW

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9839446	A2	. WO 1998-US4482	19980306
AU 9865452	A	AU 1998-65452	19980306

FILING DETAILS:

PATENT NO	KIND		PAT	TENT NO	
					۰.
AU 9865452	A	Based on	WO	9839446	

PRIORITY APPLN. INFO: US 1997-57761 19970905; US 1997-38621 19970307; US 1997-40161 19970307; US 1997-40162 19970307; US 1997-40163 19970307; US 1997-40333 19970307; US 1997-40334 19970307; US 1997-40336 19970307; US 1997-40626 19970307; US 1997-43311 19970411; US 1997-43312 19970411; US 1997-43313 19970411; US 1997-43314 19970411; US 1997-43315 19970411; US 1997-43568 19970411; US 1997-43569 19970411; US 1997-43576 19970411; US 1997-43578 19970411; US 19970411; US 1997-43669 1997-43580 19970411; US 1997-43670 19970411; US 1997-43671 19970411; US 1997-43672 19970411; US 1997-43674 19970411; US 1997-47492 19970523; US 1997-47500 19970523; US 1997-47501 19970523; US 19970523; US 1997-47503 1997-47502 19970523; US 1997-47581 19970523; US 19970523; US 1997-47583 1997-47582 19970523; US 1997-47584 19970523; US 19970523; US 1997-47586 1997-47585

19970523; US 1997-47587 19970523; US 1997-47588 19970523; US 1997-47589 19970523; US 1997-47590 19970523; US Searcher: Shears 308-4994

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19970523; US 1997-47593
1997-47592
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1997-48964
19970606; US 1997-56630
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1997-56845
19970822; US 1997-56864
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1997-56872
19970822; US 1997-56875
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             19970822; US 1997-56877
1997-56876
19970822; US 1997-56878
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19970822; US 1997-56881
                          19970822; US
1997-56882
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19970822; US 1997-56886
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1997-56887
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19970822; US 1997-56889
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             19970822; US 1997-56893
1997-56892
19970822; US 1997-56894
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1997-56903
              19970822; US 1997-56908
19970822; US 1997-56909
                           19970822; US
             19970822; US 1997-56911
1997-56910
19970822; US 1997-57650
                           19970905
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AN 1998-609887 WPIDS

CR 1998-414099 [35]; 1998-414100 [35]; 1998-414105 [35]; 1998-414114 [35]; 1998-427559 [35]; 1998-506364 [42]; 1998-520811 [44]; 1999-059865 [05]; 1999-080881 [07]; 1999-120770 [10]; 1999-132229 [11]; 1999-132234 [11]; 1999-204988 [17]; 1999-418749 [32]; 1999-430031 [36]

AB WO 9839446 A UPAB: 19990908

An isolated nucleic acid molecule (NAM) (I) comprising a polynucleotide (PN) having a nucleotide sequence (NS) at least 95% identical to:

(a) a PN fragment of one of a total of 70 defined human cDNA sequences given in the specification or a PN fragment of the cDNA sequence included in ATCC Deposit No. Z, which is

hybridisable to one of the 70 defined cDNA sequence;

- (b) a PN which is an (allelic) variant of one of the 70 defined cDNA sequences;
- (c) a PN encoding a biologically active polypeptide or a polypeptide fragment, domain or epitope of one of the 70 defined amino acid sequences given in the specification or a polypeptide fragment encoded by a cDNA sequence included in ATCC Deposit No. Z which is hybridisable to one of the defined cDNA sequence;
- (d) a PN which encodes a species homologue of one of the 70 defined polypeptides., or
- (e) a PN capable of hybridising under stringent conditions to any one of the PNs specified in (a)-(d), where the PN does not hybridise under stringent conditions to a sequence of only A residues or of only T residues.

Also claimed are:

- (1) a recombinant vector comprising (I),
- (2) a method of making a recombinant host cell comprising (1);
- (3) a recombinant host cell produced by a method as in (2):
- (4) an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from a polypeptide fragment (preferably having biological activity), domain, epitope, secreted form, full-length protein, (allelic) variant or species homologue of one of the 70 defined amino acid sequences or the encoded sequence included in ATCC Deposit No. Z;
- (5) an isolated antibody that binds specifically to an isolated polypeptide as in (4);
- (6) a recombinant host cell that expresses an isolated polypeptide as in (4), and
- (7) a gene corresponding to a cDNA sequence of the 70 defined amino acid sequences.

Note., From the disclosure 'ATCC Deposit No. Z' refers to the representative clones, each containing a subset of the defined cDNA sequences, which have been deposited with the ATCC. The deposit numbers are- ATCC 97900, 97901, 97903, 97898, 209010, 97897, 97897, 97897, 97976, 97904, 97926, 209043-209050, 209085, 209084, 209236.

USE - The PNs and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions (claimed), e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new PNs (claimed). Specific uses are described for each of the 70 PNs, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukaemias, diseases of the immune system (including allergies or asthma), lymphocytic diseases, brain associated diseases, hepatic and renal disease, lymphomas,

Searcher: Shears 308-4994

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inflammation, ischemic shock, Alzheimer's and cognitive disorders, schizophrenia, restenosis, prostate diseases, obesity, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, diseases of testis, lung or thymus, digestive/endocrine disorders, including metabolic regulation, malabsorption, gastritis and neoplasms, and AIDS. The polypeptides are also useful for identifying their binding partners (claimed).

Dwg.0/10

L6 ANSWER 10 OF 14 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD

ACCESSION NUMBER:

1998-594496 [50] WPIDS

DOC. NO. NON-CPI:
DOC. NO. CPI:

N1998-462620 C1998-178291

TITLE:

· New isolated human genes and secreted

polypeptide(s) they encode - useful for the diagnosis and treatment of e.g. cancers, CNS disorders, immune system disorders, inflammatory

disease and bacterial infections.

DERWENT CLASS:

B04 D16 S03

INVENTOR(S):

FENG, P; NI, J; ROSEN, C A; RUBEN, S M; YU, G

PATENT ASSIGNEE(S):

(HUMA-N) HUMAN GENOME SCI INC

COUNTRY COUNT:

82

PATENT INFORMATION:

PATENT NO	KIND DATE	WEEK	LA	PG

WO 9845712 A2 19981015 (199850) * EN 141

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW

W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM GW HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZW

AU 9869529 A 19981030 (199911)

APPLICATION DETAILS:

11112111 110	KIND	APPLICATION	DATE
WO 9845712	A2	WO 1998-US6801	
AU 9869529	A	AU 1998-69529	19980407

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 9869529	A Based on	WO 9845712

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PRIORITY APPLN. INFO: US 1997-48184 19970530; US 1997-42726 19970408; US 1997-42727 19970408; US 1997-42728 19970408; US 1997-42754 19970408; US 1997-42825 19970408; US 1997-48068 19970530; US 1997-48070 19970530

AN 1998-594496 [50] WPIDS

AB

WO 9845712 A UPAB: 19990210

An isolated nucleic acid molecule (NAM) (I) is claimed comprising a polynucleotide (PN) having a nucleotide sequence (NS) at least 95% identical to:(a) a PN fragment of a total of 20 defined human cDNA sequences given in the specification or a PN fragment of the cDNA sequence included in ATCC Deposit No. Z which is hybridisable to one of the 20 defined cDNA sequences; (b) a PN which is an (allelic) variant of one of the 20 defined cDNA sequence; (c) a PN encoding a biologically active polypeptide or a polypeptide fragment, domain or epitope of one of the 20 defined amino acid sequences given in the specification or a polypeptide fragment encoded by a cDNA sequence included in ATCC Deposit No. Z which is hybridisable to one of the defined cDNA sequences; (d) a PN which encodes a species homologue of one of the 20 defined polypeptides; or (e) a PN capable of hybridising under stringent conditions to any one of the PNs specified in (a) - (d), where the PN does not hybridise under stringent conditions to a sequence of only A residues or of only T residues. Also claimed are: (1) a recombinant vector comprising (I); (2) a method of making a recombinant host cell comprising (I); (3) a recombinant host cell produced by a method as in (2); (4) an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from a polypeptide fragment (preferably having biological activity), domain, epitope, secreted form, full-length protein, (allelic) variant or species homologue of one of the 20 defined amino acid sequences or the encoded sequence included in ATCC Deposit No. Z; (5) an isolated antibody that binds specifically to an isolated polypeptide as in (4); (6) a recombinant host cell that expresses an isolated polypeptide as in (4); (7) a gene corresponding to a cDNA sequence of one of the 20 nucleotide sequences given in the specification. Note: From the disclosure ''ATCC deposit No. Z'' refers to ATCC No's 97955 and 209074.

USE - The PNs and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions (claimed), e.g. by protein of gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new PNs (claimed). Specific uses are described for each of the 20 PNs, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of central nervous system (CNS) and immune system diseases, reproductive disorders, cancers,

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congenital malformations, degenerative diseases, trauma, inflammatory disease, neoplasia, metabolic disorders, diseases in testes, placenta, liver, brain and activated T cells, spleen diseases, lung diseases, heart

diseases, rhabdomyosarcoma and disorders of the endocrine system or other endocrinopathies, e.g. endocrine polyglandular syndrome, endocrinoma, and endocrine ophthalmopathy, osteoclastoma and other bone remodelling disorders, bacterial infections and sepsis. The polypeptides are also useful for identifying their binding partners (claimed).

Dwg.0/0

L6 ANSWER 11 OF 14 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD

ACCESSION NUMBER: 1998-506364 [43] WPIDS

CROSS REFERENCE: 1998-414099 [35]; 1998-414100 [35]; 1998-414105

[35]; 1998-414114 [35]; 1998-427559 [35];

1998-520811 [44]; 1998-609887 [42]; 1999-059865

[05]; 1999-080881 [07]; 1999-120770 [10];

1999-132229 [11]; 1999-132234 [11]; 1999-204988

[17]; 1999-418749 [32]; 1999-430031 [36]

DOC. NO. NON-CPI: N1998-394741 DOC. NO. CPI: C1998-152795

TITLE: New isolated human genes and the secreted

polypeptide(s) they encode - useful for diagnosis

and treatment of e.g. cancers, neurological

disorders, immune diseases, inflammation or blood

disorders.

DERWENT CLASS: B04 D16 S03

INVENTOR(S): BEDNARIK, D P; BREWER, L A; CARTER, K C; DUAN, R;

EBNER, R; ENDRESS, G A; FENG, P; FERRIE, A M; FISCHER, C L; FLORENCE, K A; GREENE, J M; HU, J; NI, J; OLSEN, H S; ROSEN, C A; RUBEN, S M; SOPPET, D R; YOUNG, P E; YU, G; KYAW, H; LAFLEUR, D W; LI,

Y; MOORE, P A; SHI, Y; ZENG, Z

PATENT ASSIGNEE(S): (HUMA-N) HUMAN GENOME SCI INC

COUNTRY COUNT: 81

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG

WO 9839448 A2 19980911 (199843)* EN 721

RW: AT BE CH DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW

NL OA PT SD SE SZ UG ZW

W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM GW HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT

LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZW

AU 9865453 A 19980922 (199908) AU 9891304 A 19990322 (199931)

AU 9891304 A 19990322 (199931)

Searcher : Shears 308-4994

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9839448	A2	WO 1998-US4493	19980306
AU 9865453	Α	AU 1998-65453	19980306
AU 9891304	A	AU 1998-91304	19980903

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 9865453	A Based on	WO 9839448
AU 9891304	A Based on	WO 9911293

PRIORITY APPLN. INFO: US 1997-61060 19971002; US 1997-38621 19970307; US 1997-40161 19970307; US 1997-40163 19970307; US 1997-40333 19970307

AN 1998-506364 [43] WPIDS

CR 1998-414099 [35]; 1998-414100 [35]; 1998-414105 [35]; 1998-414114 [35]; 1998-427559 [35]; 1998-520811 [44]; 1998-609887 [42]; 1999-059865 [05]; 1999-080881 [07]; 1999-120770 [10]; 1999-132229 [11]; 1999-132234 [11]; 1999-204988 [17]; 1999-418749 [32]; 1999-430031 [36]

AB WO 9839448 A UPAB: 19990908

An isolated nucleic acid molecule (I) comprises a polynucleotide (PN) having a nucleotide sequence at least 95% identical to: (a) a PN fragment of one of a total of 186 defined human cDNA sequences given in the specification or a PN fragment of the cDNA sequence included in ATCC Deposit No: Z, which is hybridisable to one of the 186 defined cDNA sequences; (b) a PN which is an (allelic) variant of one of the 186 defined cDNA sequences; (c) a PN encoding a biologically active polypeptide or a polypeptide fragment, domain or epitope of one of the 186 defined amino acid sequences given in the specification or a polypeptide fragment encoded by a cDNA sequence included in ATCC Deposit No. Z, which is hybridisable to one of the defined cDNA sequences; (d) a PN which encodes a species homologue of one of the 186 defined polypeptides; or (e) a PN capable of hybridising under stringent conditions to any one of the PNs specified in (a)-(d), where the PN does not hybridise under stringent conditions to a sequence of only A residues or of only T residues.

Also claimed is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from:

(a) a polypeptide fragment (preferably having biological activity), domain, epitope, secreted form, full-length protein,

(allelic) variant or species homologue of one of the 186 defined

Searcher: Shears 308-4994

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amino acid sequences or the encoded sequence included in ATCC Deposit No: Z.

Note: From the disclosure ''ATCC Deposit No: Z'' refers to the representative clones, each containing a subset of the defined cDNA sequences, which have been deposited with the American Type Culture Collection. The deposit numbers are: ATCC 97897-97904 and ATCC 209076, 209215, 209139, 209011, 209119, 209235, 209627 and 209043-209050.

USE - The polynucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions (claimed), e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides (claimed). Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of: cancer; tumours; neurodegenerative disorders; developmental abnormalities and foetal deficiencies; blood disorders; leukaemias; diseases of the immune system (including allergies or asthma); lymphocytic diseases; brain associated diseases; hepatic and renal disease; lymphomas; inflammation; ischaemic shock; Alzheimer's and cognitive disorders; schizophrenia; restenosis; prostate diseases; obesity; disorders involving osteoclasts such as osteoporosis, arthritis or malignancies; diseases of testis, lung or thymus; thyroiditis and thyroid tumours; digestive/endocrine disorders, including metabolic regulation, malabsorption, gastritis and neoplasms; and AIDS. The polypeptides are also useful for identifying their binding partners (claimed). Dwg.0/0

DERWENT INFORMATION LTD ANSWER 12 OF 14 WPIDS COPYRIGHT 1999 L6

ACCESSION NUMBER: 1998-437479 [37] WPIDS

DOC. NO. NON-CPI: N1998-340776 C1998-133112 DOC. NO. CPI:

New nucleic acid for the lung TITLE:

disease marker LU105 - polypeptides,

antibodies and genes, used for diagnosis,

prevention, treatment of lung disease, specifically cancer.

DERWENT CLASS:

B04 D16 S03

INVENTOR(S):

BILLING-MEDEL, P A; COHEN, M; COLPITTS, T L;

FRIEDMAN, P N; GORDON, J; GRANADOS, E N; HODGES, S C; KLASS, M R; KRATOCHVIL, J D; ROBERTSRAPP, L;

RUSSELL, J C; STROUPE, S D

PATENT ASSIGNEE(S):

(ABBO) ABBOTT LAB

COUNTRY COUNT:

19 PATENT INFORMATION:

> 308-4994 Searcher : Shears

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PATENT NO KIND DATE WEEK LA PG

WO 9833926 A1 19980806 (199837) * EN 117

RW: AT BE CH DE DK ES FI FR GB GR IE IT LU MC NL PT SE

W: CA JP

APPLICATION DETAILS:

PATENT NO KIND APPLICATION DATE

WO 9833926 A1 WO 1998-US1766 19980130

PRIORITY APPLN. INFO: US 1997-791710 19970131

AN 1998-437479 [37] WPIDS

AB WO 9833926 A UPAB: 19980916

A method for detecting target LU105 nucleic acid (I) comprises treating a sample with at least one LU105-specific nucleic acid (II), or its complement. (II) is at least 50% identical with 190, 244, 225, 114, 562 or 519 bp sequences given in the specification, or their fragments and complements.

Also claimed are:

- (1) (I) or its fragments able to hybridise selectively to the LU105 gene and having at least 50% identity with the 190, 244, 225, 114, 562 or 519 bp sequences given above;
- (2) recombinant expression systems including (I) and control sequence;
 - (3) cells transformed with this expression system;
- (4) LU105 polypeptides (III) at least 50% identical with the 104, 26, 19, 21, 18 or 19 amino acid (aa) sequences given in the specification or their fragments;
- (5) antibodies (Ab) that bind to at least one LU105 epitope present in (III);
- (6) cells transformed with the 190, 244, 225, 114, 562 or 519 bp sequences described above;
 - (7) LU105 specific nucleic acid (II); and
- (8) genes, or their fragments, that encode a protein at least 50% identical with the 104 aa sequences as in (4).

USE - LU105 is a lung disease marker. Cells as in (3) are used to express recombinant (III) which are used to raise Ab. Ab are used to detect the LU105 antigen, and correspondingly this antigen is used to detect specific antibodies, in usual immunoassays. (I) and (III) are used for diagnosis, staging, monitoring, prognosis, prevention, treatment (e.g. using antisense molecules, ribozymes, Ab or other antagonists) and determination of susceptibility to, lung disease, specifically cancer. (III) are also used to screen for specific binding agents, potentially useful Searcher: Shears 308-4994

therapeutically. LU105 is a marker for lung disease (present at high concentration, in altered form or in an unusual body compartment).

ADVANTAGE - LU105 can be detected in blood, plasma or serum in an inexpensive, non-invasive test.

Dwg.0/6

L6 ANSWER 13 OF 14 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD

ACCESSION NUMBER: 1998-333327 [29] WPIDS

DOC. NO. NON-CPI: N1998-260122 DOC. NO. CPI: C1998-103375

TITLE: Human chemokine beta-13 polypeptide - useful in diagnosis and treatment of immune-system related

disorders e.g. cancer of the immune system,

leukaemias, autoimmune diseases etc..

DERWENT CLASS: B04 D16 S03

INVENTOR(S): LI, H; SEIBEL, G

PATENT ASSIGNEE(S): (HUMA-N) HUMAN GENOME SCI INC

COUNTRY COUNT: 79

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG

WO 9824908 Al 19980611 (199829)* EN 86

RW: AT BE CH DE DK EA ES FI FR GB GH GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW

W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI

GB GE GH HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM

TR TT UA UG US UZ VN YU ZW

AU 9853834 A 19980629 (199845)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9824908	A1	WO 1997-US23144	19971205
AU 9853834	A	AU 1998-53834	19971205

FILING DETAILS:

PATENT NO	KIND		PAT	TENT NO
AU 9853834	A Based	on	WO	9824908

PRIORITY APPLN. INFO: US 1996-32432 19961205

AN 1998-333327 [29] WPIDS

AB WO 9824908 A UPAB: 19980722

Isolated human chemokine beta -13 (CK beta -13) polypeptide Searcher : Shears 308-4994

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comprises amino acid sequence: (a) 95 % identical or more to 93 amino acid sequence (I) given in the specification, (b) mature CK beta -13 polypeptide sequence comprising amino acids 25-93 or 29-93 of sequence (I); (c) encoded by cDNA clone contained in ATCC 97113; or (d) a sequence complementary to the sequences as in (a)-(b).

Also claimed are: (1) polypeptide comprising epitope -bearing portion of CK beta -13 protein comprising amino acids Thr22-Gly28, Asn30-Leu47, Thr56-Val65 or Phe70-Trp83 of sequence (I); (2) nucleic acid molecules as follows: (I) encoding CK beta -13 polypeptide sequences as above; (ii) complementary to (I); (iii) hybridising to (I) but not to polynucleotide with sequence consisting of only A or only T residues; (iv) encoding epitope-bearing portion of (I), optionally as in (1); (v) having 282 bp sequence (II) and optionally encoding CK beta -13 polypeptide sequences as above; (vi) at least 95 % identical to sequence encoding polypeptide with amino acids n-93, 1-m and n-m (n and m are integers between 1-35 and 77-93 respectively) of (I); and (vii) encoding polypeptide which is a portion of CK beta -13 sequence encoded by cDNA clone in ATCC 97113 excluding 1-35 amino acids from amino terminus and/or 1-17 amino acids from carboxy terminus; (3) recombinant vectors produced by inserting (I) into vector; (4) host cells produced by introducing the vector as in (4); and (5) antibody binding specifically to CK beta -13 polypeptide.

USE - The polypeptides and nucleic acids are useful in diagnosis and treatment of immune system-related disorders in mammals (preferably humans). Such disorders include tumours, cancers, interstitial lung disease and disregulation of immune cell function including leukaemias, lymphomas, autoimmune diseases etc. For example, certain tissues in mammals with cancer of the immune system express enhanced/decreased levels of CK beta -13 and mRNA encoding CK beta -13, and diagnosis can be achieved by assaying CK beta -13 gene expression and comparing to standard levels. The polypeptides can be administered therapeutically in pharmaceutical compositions e.g. to treat immune system-related disorders as above, treat sepsis, inhibit bone marrow stem cell colony formation during cancer therapy, regulate haematopoiesis, stimulate wound healing etc. Compositions comprising the polynucleotides may also be administered, especially to express CK beta -13 polypeptide in hosts to treat dysfunctions associated with aberrant endogenous CK beta -13 activity. The polynucleotides are also useful for mapping of chromosomes/chromosome sites. The polypeptides are useful to screen for agonists and antagonists of CK beta -13 activity. The antibodies are useful diagnostically or therapeutically e.g. as antagonists to treat subjects requiring CK beta -13 reduction. Dwg.0/4

L6 ANSWER 14 OF 14 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD ACCESSION NUMBER: 1998-286957 [25] WPIDS

Searcher: Shears 308-4994

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DOC. NO. NON-CPI:

N1998-225472

DOC. NO. CPI:

C1998-088988

TITLE:

Lung tissue derived polynucleotide LU103 - useful

to detect, diagnose, stage,

monitor, prognose, prevent, treat or determine pre-disposition to lung

disease, e.g. lung cancer.

DERWENT CLASS:

B04 D16 S03

INVENTOR(S):

COHEN, M; FRIEDMAN, P N; GORDON, J; HODGES, S C;

KLASS, M R; KRATOCHVILL, J D; ROBERTS-RAPP, L;

RUSSELL, J C; STROUPE, S D

PATENT ASSIGNEE(S):

(ABBO) ABBOTT LAB

COUNTRY COUNT:

19

PATENT INFORMATION:

PATENT NO KIND DATE

LA PG

WO 9820143 A1 19980514 (199825) * EN 86

WEEK

RW: AT BE CH DE DK ES FI FR GB GR IE IT LU MC NL PT SE

W: CA JP

APPLICATION DETAILS:

PATENT NO KIND

APPLICATION DATE

WO 9820143 A1

WO 1997-US20680 19971105

PRIORITY APPLN. INFO: US 1996-744211 19961105

1998-286957 [25] WPIDS AN

WO 9820143 A UPAB: 19980715 AB

The following are claimed: (1) a method for detecting the presence of a target LU103 polynucleotide in a test sample, comprising: (a) contacting the sample with at least 1 LU103-specific polynucleotide, and (b) detecting the target LU103 polynucleotide in the test sample, where the LU103 polynucleotide has at least 50% identity to the 269, 263, 225, 507 or 519 bp nucleic acid sequence given in the specification; (2) a method for detecting LU103 mRNA in a test sample, comprising: (a) performing reverse transcription with at least 1 primer in order to produce cDNA; (b) amplifying the cDNA using LU103 oligonucleotides as sense and antisense primers to obtain LU103 amplicon, and (c) detecting LU103 amplicon in the test sample, where the LU103 oligonucleotides utilised in steps (a) and (b) have at least 50% sequence identity to the 269, 263, 225, 507 or 519 bp sequence and (3) a method detecting a target LU103 polynucleotide in a test sample suspended of containing the target, comprising: (a) contacting the test sample with at least 1 LU103 oligonucleotide as a sense primer and at least 1 LU103 oligonucleotide as an anti-sense primer and amplifying to obtain a Searcher : Shears 308-4994

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first stage reaction product; (b) contacting the first stage reaction product with at least 1 other LU103 oligonucleotide to obtain a second stage reaction product, provided that the other LU103 oligonucleotide is located 3' to the LU103 oligonucleotides utilised in step (a) and is complementary to the first stage reaction product, and (c) detecting the second stage reaction product as an indication of the presence of the target LU103 polynucleotide, where the LU103 oligonucleotides utilised in steps (a) and (b) have at least 50% sequence identity to the 269, 263, 225, 507 or 519 bp sequence; (4) a purified polynucleotide derived from an LU103 gene, where the polynucleotide is capable of selectively hybridising to the nucleic acid of the LU103 gene and has at least 50% identity to the 269, 263, 225, 507 or 519 bp sequence; (5) a recombinant expression system comprising a nucleic acid sequence that includes an ORF derived from LU103 operably linked to a control sequence compatible with a desired host, where the nucleic acid sequence has at least 50% identity to the 269, 263, 225, 507 or 519 bp sequence; (6) cell transfected with the recombinant expression system; (7) cell transfected with a nucleic acid sequence encoding at least 1 LU103 epitope, where the nucleic acid sequence has the 269, 263, 225, 507 or 519 bp sequence; (8) composition comprising a LU103 polynucleotide, where the polynucleotide has at least 50% identity to the 269, 263, 225, 507 or 519 bp sequence; (9) gene which encodes a LU103 protein which comprises an amino acid sequence with at least 50% identity with the 93 residue amino acid sequence given in the specification, and (10) gene comprising DNA having at least 50% identity with the 507 or 519 bp sequence.

USE - The methods and products of the invention may be used to detect, diagnose, stage, monitor, prognose, prevent, treat or determine the predisposition diseases and conditions of the lung, e.g. lung cancer.

Dwg.0/4

(FILE 'USPATFULL' ENTERED AT 12:18:19 ON 25 OCT 1999)
7 S L2(S) (REAGENT OR EPITOPE OR LS147 OR LS 147)

L9 ANSWER 1 OF 7 USPATFULL

ACCESSION NUMBER:

1999:96216 USPATFULL

TITLE:

L9

Reagents and methods useful for

detecting diseases of the

lung

INVENTOR(S):

Cohen, Maurice, Highland Park, IL, United States Friedman, Paula N., Deerfield, IL, United States Gordon, Julian, Lake Bluff, IL, United States Hodges, Steven C., Buffalo Grove, IL, United

States

Klass, Michael R., Libertyville, IL, United

States

Kratochvil, Jon D., Kenosha, WI, United States Roberts-Rapp, Lisa, Gurnee, IL, United States Russell, John C., Kenosha, WI, United States Stroupe, Steven D., Libertyville, IL, United

States

PATENT ASSIGNEE(S):

Abbott Laboratories, Abbott Park, IL, United

States (U.S. corporation)

NUMBER DATE

PATENT INFORMATION:

US 5939265 19990817

APPLICATION INFO.:

US 1997-964725 19971105 (8)

RELATED APPLN. INFO.:

Continuation-in-part of Ser. No. US 1996-744211,

filed on 5 Nov 1996, now abandoned

DOCUMENT TYPE:

Utility

PRIMARY EXAMINER:
ASSISTANT EXAMINER:

Degren, Nancy Wang, Andrew

LEGAL REPRESENTATIVE:

Becker, Cheryl L.; Goller, Mimi C.

NUMBER OF CLAIMS:

21

EXEMPLARY CLAIM: NUMBER OF DRAWINGS:

6 Drawing Figure(s); 6 Drawing Page(s)

LINE COUNT:

3052

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

As set of contiguous and partially overlapping RNA sequences and polypeptides encoded thereby, designated as LU103 and transcribed from lung tissue is described. A fully sequenced clone representing the longest continuous sequence of LU103 is also disclosed. These sequences are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining the predisposition of an individual to diseases and conditions of the lung such as lung cancer.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

INCL INCLM: 435/006.000

INCLS: 435/172.300; 435/320.100; 435/325.000; 536/023.100;

536/023.500

NCL NCLM: 435/006.000

NCLS: 435/320.100; 435/325.000; 536/023.100; 536/023.500

L9 ANSWER 2 OF 7 USPATFULL

ACCESSION NUMBER:

INVENTOR (S):

1999:43653 USPATFULL

TITLE:

Amidinohydrazones as protease inhibitors Soll, Richard M., Lawrenceville, NJ, United

States

Lu, Tianbao, Exton, PA, United States

Fedde, Cynthia L., Warrington, PA, United States

Tomczuk, Bruce E., Collegeville, PA, United

States

Illig, Carl, Phoenixville, PA, United States

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DATE

NUMBER

PATENT INFORMATION: US 5891909 19990406
APPLICATION INFO.: US 1997-828160 19970327 (8)

PRIORITY INFORMATION: US 1996-14317 19960329 (60)

DOCUMENT TYPE: Utility

PRIMARY EXAMINER: Richter, Johann ASSISTANT EXAMINER: Oswecki, Jane C.

LEGAL REPRESENTATIVE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

NUMBER OF CLAIMS: 76
EXEMPLARY CLAIM: 1
LINE COUNT: 5001

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

Amidino and benzamidino compounds, including compounds of the formula: ##STR1## wherein R.sup.1 -R.sup.4, R.sup.6 -R.sup.9, Y, Z, n and m are set forth in the specification, as well as hydrates, solvates or pharmaceutically acceptable salts thereof, that inhibit proteolytic enzymes such as thrombin are described. Also described are methods for preparing the compounds of Formula

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

INCL INCLM: 514/517.000

INCLS: 514/309.000; 514/312.000; 514/345.000; 514/361.000; 514/401.000; 514/406.000; 514/518.000; 514/530.000; 514/567.000; 514/632.000; 546/141.000; 546/172.000; 546/290.000; 548/127.000; 548/353.100; 548/367.100; 549/230.000; 558/056.000; 560/303.000; 562/431.000;

562/432.000; 564/228.000

NCL NCLM: 514/517.000

NCLS: 514/309.000; 514/312.000; 514/345.000; 514/361.000; 514/401.000; 514/406.000; 514/518.000; 514/530.000; 514/567.000; 514/632.000; 546/141.000; 546/172.000; 546/290.000; 548/127.000; 548/353.100; 548/367.100; 549/230.000; 558/056.000; 560/303.000; 562/431.000; 562/432.000; 564/228.000

L9 ANSWER 3 OF 7 USPATFULL

ACCESSION NUMBER: 1998:157475 USPATFULL

TITLE: Hybridomas producing monoclonal antibodies to new

mucin epitopes

INVENTOR(S): Linsley, Peter S., Seattle, WA, United States

Horn, Diane, Seattle, WA, United States Searcher: Shears 308-4994

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Brown, Joseph P., Seattle, WA, United States PATENT ASSIGNEE(S): Sanofi, Paris, France (non-U.S. corporation)

NUMBER DATE

PATENT INFORMATION: US 5849876 19981215 APPLICATION INFO.: US 1994-179875 19940111 (8)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1992-913740, filed on

14 Jul 1992, now abandoned which is a

continuation of Ser. No. US 1987-104511, filed on

8 Oct 1987, now abandoned which is a

continuation-in-part of Ser. No. US 1986-932781,

filed on 19 Nov 1986, now abandoned

DOCUMENT TYPE: Utility

PRIMARY EXAMINER: Scheiner, Laurie

LEGAL REPRESENTATIVE: Merchant, Gould, Smith, Edell, Welter & Schmidt

NUMBER OF CLAIMS: 3 EXEMPLARY CLAIM: 1

NUMBER OF DRAWINGS: 5 Drawing Figure(s); 5 Drawing Page(s)

LINE COUNT: 1849

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

Novel hybridoma cell lines producing monoclonal antibodies reactive with purified mucin antigens from normal and tumor sources are generated using mucins, including purified mucins from tumor sources. Epitopes on mucin antigens from normal and tumor

SOUPPLICATION INFO.: US 1996-698401 19960815 (8)

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 1995-536939,

filed on 29 Sep 1995, now abandoned

DOCUMENT TYPE: Utility

PRIMARY EXAMINER: Ivy, C. Warren
ASSISTANT EXAMINER: Covington, Raymond

LEGAL REPRESENTATIVE: Sterne, Kessler Goldstein & Fox P.L.L.C.

NUMBER OF CLAIMS: 49
EXEMPLARY CLAIM: 1
LINE COUNT: 4363

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

Compounds of the formula: ##STR1## wherein R.sup.1 --R.sup.4, R.sup.7 --R.sup.8, R.sup.a, R.sup.b, R.sup.c, Y, Z, n and m are set forth in the specification, as well as hydrates, solvates or pharmaceutically acceptable salts thereof, that inhibit a number of proteolytic enzymes are described. Also described are methods for preparing the compounds of Formula I.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

INCL INCLM: 514/255.000

INCLS: 514/317.000; 514/330.000; 514/331.000; 514/603.000; 514/604.000; 514/634.000; 514/822.000; 544/398.000; 544/399.000; 544/400.000; 544/402.000; 546/021.000;

546/229.000; 546/230.000; 546/231.000; 564/237.000

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NCL NCLM: 514/255.000

NCLS: 514/317.000; 514/330.000; 514/331.000; 514/603.000;

514/604.000; 514/634.000; 514/822.000; 544/398.000; 544/399.000; 544/400.000; 544/402.000; 546/021.000; 546/229.000; 546/230.000; 546/231.000; 564/237.000

L9 ANSWER 5 OF 7 USPATFULL

ACCESSION NUMBER: 1998:69171 USPATFULL
TITLE: Cell cycle regulatory gene

INVENTOR(S): Sidransky, David, Baltimore, MD, United States
PATENT ASSIGNEE(S): The Johns Hopkins University School of Medicine,

Baltimore, MD, United States (U.S. corporation)

NUMBER DATE

PATENT INFORMATION: US 5767258 19980616 APPLICATION INFO.: US 1995-439962 19950512 (8)

DOCUMENT TYPE: Utility

PRIMARY EXAMINER: Elliot, George C. ASSISTANT EXAMINER: McGarry, Sean

LEGAL REPRESENTATIVE: Fish & Richardson, P.C.

NUMBER OF CLAIMS: 9 EXEMPLARY CLAIM: 1

NUMBER OF DRAWINGS: 5 Drawing Figure(s); 3 Drawing Page(s)

LINE COUNT: . 1506

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A novel cell cycle regulatory gene called 5'ALT is disclosed.

Methods for determining mutations or polymorphisms in 5'ALT or
5'ALT regulated genes in tissues are also provided. Novel
5'ALT-p16 and 5'ALT-p15 transcripts and truncated expression

products are also described.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

INCL INCLM: 536/023.100

INCLS: 536/023.500; 435/006.000; 435/172.100; 435/320.100;

435/325.000; 435/243.000

NCL NCLM: 536/023.100

NCLS: 435/006.000; 435/243.000; 435/320.100; 435/325.000;

536/023.500

L9 ANSWER 6 OF 7 USPATFULL

ACCESSION NUMBER: 85:8964 USPATFULL

TITLE: .alpha.-Aminoboronic acid peptides

INVENTOR(S): Shenvi, Ashokkumar B., Wilmington, DE, United

States

Kettner, Charles A., Wilmington, DE, United

States

PATENT ASSIGNEE(S): E. I. Du Pont de Nemours and Company, Wilmington,

DE, United States (U.S. corporation)
Searcher: Shears 308-4994

NUMBER DATE

PATENT INFORMATION: US 4499082 19850212
APPLICATION INFO.: US 1983-558362 19831205 (6)

DOCUMENT TYPE: Utility

PRIMARY EXAMINER: Phillips, Delbert R. LEGAL REPRESENTATIVE: Hallquist, Scott G.

NUMBER OF CLAIMS: 19 EXEMPLARY CLAIM: 1

NUMBER OF DRAWINGS: 3 Drawing Figure(s); 3 Drawing Page(s)

LINE COUNT: 1528

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Peptides comprising C-terminal .alpha.-aminoboronic acid residues

are potent, reversible inhibitors of proteolytic enzymes.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

INCL INCLM: 514/002.000

INCLS: 260/112.500R; 514/018.000; 514/019.000

NCL NCLM: 514/002.000

NCLS: 260/001.000; 514/018.000; 514/019.000; 514/506.000;

530/331.000; 562/007.000; 930/010.000; 930/023.000;

930/250.000

L9 ANSWER 7 OF 7 USPATFULL

ACCESSION NUMBER: 85:3359 USPATFULL

TITLE: Determination of oxidized .alpha.-1-proteinase

inhibitor in serum or plasma

INVENTOR(S): Travis, James, Athens, GA, United States

PATENT ASSIGNEE(S): University of Georgia Research Foundation, Inc.,

Athens, GA, United States (U.S. corporation)

NUMBER DATE

PATENT INFORMATION: US 4493891 19850115 APPLICATION INFO.: US 1982-402442 19820727 (6)

DOCUMENT TYPE: Utility

PRIMARY EXAMINER: Kepplinger, Esther M.

LEGAL REPRESENTATIVE: Oblon, Fisher, Spivak, McClelland & Maier

NUMBER OF CLAIMS: 13 EXEMPLARY CLAIM: 1

NUMBER OF DRAWINGS: 2 Drawing Figure(s); 1 Drawing Page(s)

LINE COUNT: 603

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A new method of determining oxidized .alpha.-1-proteinase inhibitor in serum or plasma for use in studying the development of chronic obstructive lung disease is disclosed. Levels of oxidized .alpha.-1-proteinase inhibitor indicate the potential for emphysema development with higher levels showing a decrease in

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lung protection against elastolytic enzymes such as elastase. This method can be used for patients with a potential for chronic obstructive lung disease rather than having to use bronchial lavage methods for such patients. No other method is known to exist for determining oxidized .alpha.-1-proteinase inhibitor in serum or plasma.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

INCLM: 435/023.000

INCLS: 435/184.000

NCL

NCLM: 435/023.000 NCLS: 435/184.000

(FILE 'CAPLUS, MEDLINE, BIOSIS, EMBASE, LIFESCI, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, PROMT, CANCERLIT, USPATFULL' ENTERED AT 12:20:18 ON 25 OCT 1999)

	12:20:18 ON 25 OCT 199	99)
L10	TO I DIM ADD-ON	PLU=ON (BILLING MEDEL P? OR BILLING P? OR
	MEDEL P? OR	R MEDEL BILLING P?)/ATT
L11	26222 SEA ABB=ON	PLU=ON COHEN M?/AU
L12	123 SEA ABB=ON	PLU=ON COLPITTS T?/AU
L13	2767 SEA ABB=ON	PLU=ON FRIEDMAN P?/AU
L14	262 SEA ABB=ON	PLU=ON KLASS M?/AU
L15	12902 SEA ABB=ON	PLU=ON RUSSELL J?/AU
L16	310 SEA ABB=ON	
L17		PLU=ON L10 AND L11 AND L12 AND L13 AND L14
	AND L15 AND	L16
L18		PLU=ON L10 AND (L11 OR L12 OR L13 OR L14 OR
	L15 OR L16)	THE SERVICE CONTRACTOR LITTER OR LIT
L19		PLU=ON L11 AND (L12 OR L13 OR L14 OR L15)
L20	51 SEA ABR=ON	PLU=ON L12 AND (L13 OR L14 OR L15)
L21	62 SEA ARREON	PLU=ON L13 AND (L14 OR L15)
L22	59 SEA ABB=ON	DIU-ON 114 AND 145
	os our red-on	PLO=ON L14 AND L15
L26	7 SEA ARR-ON	DIU-ON /III OR TIO OF THE
	L22) AND L1	PLU=ON (L17 OR L18 OR L19 OR L20 OR L21 OR
L27		
/	4 DOE KEM L26	(3 DUPLICATES REMOVED)

	-As	

1

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FEATURES
                                                                                              Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                          source
12 TGCCACTATGGGGTCTGGGCTGCCCCTT 40
                       8 TGGCCACTGGGGGGCCTGGGCTGCCCCTT 36
                                                                         n 12.8%;
Similarity 89.7%;
26; Conservative
                                                                                                                                                                                                                                                                                                                                                          Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: Mi3 Reverse.
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Pred. NO. 3.57e-06;
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                                                                                                                                                              64 t
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                                                                                                    Length 311;
                                                                                                                                                            4 others
                                                                 Gaps
                                                               0
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                            Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Manmalla; Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Manmalla; Eukherla; Primates; Catarrhini; Hominidae; Homo.

2E 1 (bases 1 to 311)

RS Adams, M.D. Rerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Buit, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., Mitte, O., Sutton, G., Blake, J.A., Brandon, R.C., Manwai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodék, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Milly, C.A., Ryder, S.E., Scott, J.L., Sadek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Hednarik, D.F., Forzigs, A., Coleman, T.A., Collins, E.J., Dimke, D., Fengo, D.-F., Ferrite, A., Fischer, C., Hastings, G.A., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Millon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, M.A., Fields, C., Initlal assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

NE 96086280

On Ant 14 1003 + His carmano, varrian variance.
On Apr 14, 1993 this sequence version replaced gi:693635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA323964 311 bp mRNA EST
EST26816 Cerebellum II Homo sapiens cDNA 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA323964.1 GI:1976290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-APR-1997
end, mRNA sequence.
```

Contact: Kerlavage, AR Bioinformatics The InStitute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA

RESULT 10
LOCUS
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DEFINITION ACCESSION AA323964
NID g1976290
VERSION AA323964.1 GI:1976290
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 311)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., weidman, J.F., Li, Y., Bednarlk, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,

Mon Oct 25 11:53:39 1999

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Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
96026280
On Apr 14, 1993 this sequence version replaced the Costa
      TITLE
      JOURNAL
      MEDLINE
                                       On Apr 14, 1993 this sequence version replaced g1:693635.
COMMENT
                                     Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlavetigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.

Location/Oualifiers
1. 311
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88888888888888888888888888888888
                            SOFTWARE: PC-DOS/NS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/418,444A
FILING DATE: 07-APR-1995
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: JP HEI 6-71048
FILING DATE: 08-APR-1994
ATTORNEY/AFENT INFORMATION:
NAME: Oblon, NO. 573568man F.
REGISTRATION NUMBER: 24,618
REFERENCE/POCKET NUMBER: 2589-024-0
TELEFAR: (703) 413-3000
TELEFAR: (703) 413-3200
TELEFAR: (703) 413-3200
TELEFAR: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3088 base pairs
TYPE: nucleic acid
STANDEDNESS: double
TOPOLOGY: 11-02-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-418-444A-1 STANDARD; DNA; UNC; 3088 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/0841844A Sequence 1, Application US/0841844A Patent No. 5773688
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UPPLICANT: KURODA, HISAO
UPPLICANT: HIROTA, NAOHIKO
UPPLICANT: ITO, KAZUTOOSHI
ITILE OF INVENTION: CENE EXPRES
ITILE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENE EXPRESSION VECTOR USING THE GENE EXPRESSION REGULATING REGION OF THE ADP RIBOSYLATION
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Query Match
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local Similarity 72.0%;
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Pred. No. 1.54e-01;
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90 CCAAGGAGGGTCAAGAGGAGACAAGGGGCAGCCCCAGACCCCATAGTGGC 41

a

			ilė,
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Gaps
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Sequence 1, Application US/08418444A

C Sequence 1, Application US/08418444A

CC Patent No. 5713688

CC GENERAL INFORMATION:
CC APPLICANT: TURONA, HISAO
CC APPLICANT: TURONA, HOSAU
CC APPLICANT: TYO, KAZUTOSHI
CC TITLE OF INVENTION: GENE EXPRESSION VECTOR USING THE GENE
CC TITLE OF INVENTION: EXPRESSION VECTOR USING THE ADP RIBOSYLATION
CC TITLE OF INVENTION: FACTOR
CC NUMBER OF SEQUENCES: 9

CC NUMBER OF SEQUENCES: 9

CC CORRESPONDENCE ADDRESS:
CC NUMBER OF SEQUENCES: 9

CC STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CC STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CC STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CC COMPUTER READABLE FORM:
CC SOFTWARE: PATENTIAN FORDS/MS-DOS

CC SOFTWARE: PATENTIAN SUSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PATENTIAN SUSTEM: PC-DOS/MS-DOS

CC CURRENT APPLICATION NOWBER: US/08/418,444A

CC CORREST APPLICATION NOWBER: JP HEI 6-71048

FILING DATE: 08-APR-1994

CC APPLICATION NUMBER: JP HEI 6-71048

FILING DATE: 08-APR-1994

CC APPLICATION NUMBER: 24.618

CC PRIOR APPLICATION INFORMATION:
CC TELECOMUNICATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-418-444A-1 STANDARD; ONA; UNC; 3088 BP.
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 3088 BP; 716 A; 761 C; 672 G; 939 T; 0 OTHER. TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3088 base pairs

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Ouery Match 12.2%; Score 22; DB 3; Length 3088; Best Local Similarity 72.0%; Pred. No. 7.70e-02; Matches 36; Conservative 0; Mismatches 14; Indels

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